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Result
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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2: pir2:*
3: pir3:*
4: pir4:*
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133	134	134	138.5	138.5	139.5	142	142	142	147.5	147.5	152.5	153	161	162	189.5
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356	825	801	749	353	288	687	356	356	598	329	324	254	1316	283	880
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hypothetical prote	hypothetical prote	hypothetical prote	probable membrane	conserved hypothet	probable aspartate	PepA protein - Pse	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	conserved hypothet	hypothetical UPF00	probable phosphoes	hypothetical prote

ALIGNMENTS

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70420 conserved hypothetical protein aq_1386 - Aquifex aeolicus C;Species: Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999 C;Accession: F70420 A; Experimental source: strain C; Genetics: A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: CAOF A;Residues: 1-259 - AOF A;Cross-references: GB:A5000737; NID:g2983782; PIDN:AAC07357.1; PID:g2983799; GB:AE00A;Cross-references: GB:A5000737; NID:g2983782; PIDN:AAC07357.1; PID:g2983799; GB:AE00A;ACC07357.1; PID:g2983790; GB:AE00A;ACC07357.1; PID:g2983799; GB:AE00A;ACC07357.1; PID:g2983790; GB:AE00A;ACC0737.1; PID:g2983790; GB:AE00A;ACC0737.1; PID:g2983790; GB:AE00A;ACC0757.1; PID:g2983790; GB:AE00A;ACC0757.1; PID:g2983790; GB:AE00A;ACC0757.1; PID:g2983790; GB:g298790; GB:AE00A;ACC07570; GB:AE00A;ACC07570; GB:AE00A;ACC07570 뫄 Ś 밁 δ 맑 Ś 片 S 밁 A;Gene: aq_1386 Nature 392, 353-358, 1998 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, Query Match Best Local Similarity Matches 178; 185 125 121 RALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEPFQESGIPTVCVDV 180 245 GYESTLRIM 241 GYIKALEVL 249 \$3 19 LPIEPEKDIKNILHILLERSFFLAVRSNSEKRKEFCDLVIVPELBEFTPLDVRKADQIMER GMFSLLKRVNWLKLFKFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICATDLYSG EMLKLLKEVNWLKLFKFKTPKMGLMGWEKAAEFLEKELGVKRLEDLNIPTYLCSADLYTG LPITQERKIKNILHILIRSFFLAVRSNSEKRKEFCNVVIEPPLEEFSPLDVNKADEIFLR KALYFGRGDLIPVLIGSCSIPGIFEPVEYENFLLVDGGIVNNLFVEFLEKFKEFIIGVDV Conservative 253 73.4%; VF5 31; Mismatches Score 934; DB 2; Pred. No. 9.9e-74; 40; Length 259; Indel.s 0, Gaps 240 184 244 124 120 64 0 D.E.

RESULT 2

883228

kypothetical protein PA3339 [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change C;Accession: E83228

C;Accession: E83228
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener,

#text_change 31-Dec-2000

P.; Hickey,

м.ј.;

(strain

PAO1

us-09-903-410-36.rpr

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                                          184 EPEKDIKNILHILLRSPFLAVRSNSEKRKEFCDLVIVPELEEFTPL 229
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Les 79; Conserv
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A;Molecule type: DNA
A;Residues: 1-764 <HEI>
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Matches 79,
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R;Takahi, H.; Nakasone, K.; Takahi, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
R;Takami, H.; Nakasone, K.; Takahi, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4317, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUD:20512582; PMID:11058132
A;Accession: C83973
A;Accession: C83973
A;Accession: C83973
A;Molecule type: DNA
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                       A,Cross-references: GB:AE004756, GB:AE004091; NID:g9949466; PIDN:AAG06727.1; GSPDB:GN001
A,Experimental source: strain PA01
A,Genetics:
A,Gene: PA3339
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A;Experimental source: strain C-125
                                                                                                                 an opportunistic patho
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                                                                                         A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, A;Reference number: A92950; MUID:20437337; PMID:10984043 A;Accession: E83228 A;Status: preliminary A;Status: preliminary A;Residues: 1-728 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 728;
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Serine proteinase (EC 3.4.21.-) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Accession: AB3639
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov. Maccolla meliter proc. Natl. Acad. Sci. U.S.A. 99, 433-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melite A;Accession: AB3639
A;Status: preliminary
A;Reference number: AD3252; PMID:11756688
A;Status: preliminary
A;Residues: 1-233 ckTR.>
A;Cross-references: GB:AE008918; PIDN:AAL54277.1; PID:G17985253; GSPDB:GN00191
C;Genetics:
A;Genetics:
A;Map position: II
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross_references: GB;AE004145; GB;AE003852; NID:g9655032; PIDN:AAF93770.1; GSPDB;GN
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
                                                                                                                                 Gwinn, M.L.; Dodson, R.
H.; Dragoi, I.; Sellere
   ser
                             C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Jate: Ile-Ang-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: B82303
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, Chardson, D.; Ermoiaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Selle N. R. : Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
conserved hypothetical protein VC0603 [imported] - Vibrio cholerae (strain N16961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 IRFLEEV---LP-YRRIEKLEIPTYICATDLYSGRALYLSEGSLIPALLGSCAIPGIFEP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 QVAKRPKIALVLAGGGAKGAAHMGVLRALEEMHVPVDIITGTSMGAYVGGLYATGMSAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PKPPLKGLIGWEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 VEYKNYLLVDGGIVNNLPVEPFQESGIP-TVCVDV-LPIEPEKDIKNILHILLRSFFLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RLRKFEEINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.4%; Score 297.5; DB 2; Length 764; 27.6%; Pred. No..8.8e-18; tive 61; Mismatches 105; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 RSNSEKRKEPC---DLVIVPELEEFTPLDVRKADQIMERGYIKALE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ::|:: | | : | |:: | 267 RRSTERQSDHLTSRDLLLRPPVGKMETMEFDKMPAAFAMGYQEAMD 312
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conserved hypothetical
C;Species: Agrobacteriv
C;Date: 11-Jan-2002 #s
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A;Cross-references: GB:AL162752; GB:AL157959; NID:G7378778; PIDN:CAB83536.1; A;Experimental source: serogroup A, strain Z2491
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mor
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrea
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A82017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable lipoprotein NMA0225 [imported] - Neisseria meningitidis (strain Z2.C;Species: Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: A82017
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                                                                                                                                                                                                                                                                                                                                                                                                                           Match 21.6%; Score 274.5; DB 2; Local Similarity 31.8%; Pred. No. 2.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NMA0225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
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                                                                                                                                                                                                                                                                  106 LGKTDLVDLTLSTSGFIKGEKLQNYINRKVGGRRIQQFPIKFAAVATDFETGKAVAFNQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73
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             Agrobacterium tumefaciens
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                                                                                                                                                                                                                                                                                                                                      RIGLLDFLKFEQVISQ 262
                                                                                                                                                                                                                               SLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEPFQESGIPTVCVDVLPIEPEKD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFTPLDVRKADQIMER 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTYICATDLYSGRALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEPF 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THRSEVVRRMWQTRPAHWAELFK-----GGLRVSQFHIEKVLDVFLPDSFP-SHVEDLKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAFGGGGARGIAHIHVVDVLNELGIQPVAIAGSSIGSIIGSSMANGMSGKDIYDYMASIF
                                                                                                                                                            IKNILHILLRSFF----LAVRSNSEKRKEF--CDLVIVPEL
                                                                                                                                                                                             NAGQAVRASAAI PNVFQPVI I GRHTYVDGGLSQPVFVSAARRQGANFVI AVDISARPSKN
                                                                                                                                                                                                                                                                                                    VNWLKLEKFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICATDLYSGRALYLSEG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDKADIVIGIDVVGGPVGPDDHMPTTFEAVIGTSQLTMCSIIENKFRYRPPHIFVRPNVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PITITAVDFHGAREIHISDGDLRSAIAASCAIPPVFAPVRRNGRILVDGGLFNPVPFDLL 186
                                                                                                                            IS-----
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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 #sequence_revision 11-Jan-2002
                                                                                                                          -QGFFSYLDQTLNVMSVSALQNELGQADVVIKPQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 276; DB :
Pred. No. 2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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    Agrobacterium tumefaciens

#text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                             Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 300;
                                                                                                                          261
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Rajandream,
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C;Accession: AH2791
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McC; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Ka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; PMID:11743193 A;Accession: AH2791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE008688; PIDN:AAL42750.1; PID:g17740191;
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Gene: Atu1751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOCAT
                                                195 ILLRSFFLAVRSNSEKRKEFCDLVIVPELEEFTPLDVRKADQIMERGY 242
                                                                                                    203 VVAVNLNYDLFGRSAVVKHAASPQGGGTPPAETAPRPGLPGVMVQAFNI1QDR-----
                                                                                                                                                                                                          143 ELRTGHEVWIHQGDLVTÄLRSSYÄLPGIFEPVQCNGRTLIDGALVNPVPVSVCRAYEQAL
                                                                                                                                                                                                                                                                 116 DLYSGRALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPV----
                                                                                                                                                                                                                                                                                                              83 LDELEBFARSLIMRRIAGLLDLTIGGGGLFGGMRLTKRMQEHLEGLRVENLEHPFIAVAT
                                                                                                                                                                                                                                                                                                                                                                     69 VNWLKLFKFKPPLK-------GLIGWEKAIRFLEEVLPYRRIEKLEIPTYICAT
                                                                                                                                                                                                                                                                                                                                                                                                                        34 IALALGGGAARGWAHIGVLRALDEAGVKIGMIAGTSIGALVGGCYLAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 INLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGMESLLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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- ISRSRLAGDPPDLMLHPRINDIGLSEFHRASEAIDRGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 273; DB 2; 1
Pred. No. 3.9e-16;
7; Mismatches 84;
                                                                                                                                                       -EPFQESGIPTVCVDVLPIEPEKDIKNILH
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293
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밁 8 R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Nujer, C.; Los, T.; Ivano', Mazur, M.; Goltsman, B.; Selkoy, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melii serine proteinase (BC 3.4.21.-) [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002 A; Accession: AF3365 A; Reference number: AD3252; , Molecule type: DNA ;Cross-references: GB:AE008917; PIDN:AAL52089.1; PID:g17982860; Residues: 1-314 <KUR> ;Status: preliminary Query Match Best Local (;Keywords: hydrolase; serine proteinase Map position: ;Experimental source: Accession: AF3365 Gene: BMEI0908 Genetics: 33 QKIALALGGGAARGWAHIGVLRALDEAGIEIEMIAGTSIGALVGGCYLAGKLNELEEFAR 7 BEINLVLSGGAAKGIAHIGVLKAINBLGIRVRALSGVSAGAIVSVFYASGYSPB-----Similarity 21.4%; Score 273; DB 2 ilarity 27.8%; Pred. No. 4e-16; Conservative 52; Mismatches strain 16M PMID:11756688 DB 2; Length 314; 98; Indels 58; GSPDB:GN00190 92

us-09-903-410-36.rpr

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9 INLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGMFSLLKR
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date. Cb.Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: H69874 *
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Bruislet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Bhrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical 34.4K protein in hnr-puru intergenic region [imported] - Agrobacterium tume Cispeciaes. Agrobacterium tumefaciens Cispeciaes. 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 Ciscession: H97570 Rigodiner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2338, 2001 A; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A; Recession: H97570 A; Ascossion: H97570 A; Ascossion: H97570 A; Status: preliminary A; A; Molecule type: DNA A; A; Molecule type: DNA A; Molecule type: Molecule typ
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A;Residues: 1-315 <KUR>
A;Cross_references: GB;AE007869; PIDN:AAK87521.1; PID:g15156852; GSPDB:GN00169
----GMPSLLKRVNWLKLPKFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICAT 115
                                                                SLTRRRAFNLLD-----ITFRG--SGLFGGMKLDGRLREHLDGIRIEDLPRFFVAVCT 143
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                                                                                                                                                                                                                                                                                                                                                                                                                       SNSEKRIC - BFCDLVIVPELEEFTPLDVRKADQIMERGYIKALEVLSE 251
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Ga. iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, P. Koetter, P.; Koningstein, G.; Kragh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardina A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Man Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porrett Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadio, T.; Sato, T.; Scanl A;Authors: Schleich, S.; Schreeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Statuston, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyi T.; Minters, P.; Wipat, A.; Yamanoto, H.; Yamano, K.; Yasumotoo, K.; Yata, K.; Yoshida, A;Authors: Yoshikawa, H.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Yoshida, A;Authors: Yoshikawa, H.; Danchin, A.; A; Yamanoto, H.; Yamano, K.; Yasumotoo, K.; Yata, K.; Yoshida, A;Accession: H68974
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Residuse: Dreliminary; nucleic acid sequence not shown; translation not shown A;Residuse: 1-260 «KUN»
A;Cross-references: GB:Z99111; GB:AL009126; NID:92633699; PIDN:CAB13377.1; PID:e1185(G6netics: A;Genetics:
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strain MC58.
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C; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Accession: A81000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C; Accession: A81002
R; Tettelin, H; Sauders, N.U.; Heidelberg, O; D; Teffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.D.; White, O.; Fleischmann, R.D.; Dougherty, E. Hickey, E.K.; Haft, D.H.; Salzberg, S.D.; White, O.; Fleischmann, R.D.; Dougherty, B. A; A.N. 1809 Hist., A. Gill, J. Scarlato, V.; Masignani, V.; Pizza, M. Schathors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A; Reference number: A81000; MUID:20175755; PMID:10710307
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B, strain MC58
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Best Local Similarity 28.2%; Pred. No. 7.7e-16;
Matches 68; Conservative 54; Mismatches 106; Indels 13;
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A)Cross-references: GB:AE002562;
A;Experimental source: serogroup C;Genetics:
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A;Experimental source: strain 9a5c

A;Experimental source: strain 9a5c

R;Simpson, A,J.G.; Redinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer,

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer,

as-Neto, B.; Docena, C.; Bl-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A,Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, B.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.F.; Marino, C.L.; Marques, M.V.; Martins,

A,Authors: Martins, E.M.F.; Matsbuuma, A.V.; Menck, C.F.M.; Miracca, B.C.; Miyaki, C.Y.

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa

A,Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei

A,Buthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei

A,Buthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei

A,Buthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei

A,Buthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei

A,Buthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei

A,Buthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.C.; da Silva, A.C
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R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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A;Residues: 1-395 <S
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                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                              153 AVAMDESNIRDLRFFS-----GGLVQGQKLQNYVNELVGKRPIEKLNKFFGAIATRLEDG 207
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                                                                                                                                              ISSKATGKNPGGLVGTVNQSISIMGQHLGEAELKRANIVIHPKVLDIGSTDFDQRNAAIL
                                                                                                                                                                                                                     VLPIEPEKDIKNILHILLRSFFLAVRSNSEKRKEFCDLVIVPELEEFTPLDVRKADQIME 239
                                                                                                                                                                                                                                                                                                    QRIMFVRGNVGEAVRASCSIPGVFEPVTIGAYHYVDGGITSPVPVDAVRQLGADFVIAVD
                                                                                                                                                                                                                                                                                                                                                                       RALYLSBGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEPFQESGIP-TVCVD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----VNWLKLFKFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICATDLYSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGIALGGGAAKGFAHIGVLKMLEANGLAPSVVAGTSAGSVVGALYASGMD---SFKIQTK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGVSPEGMFSLLKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGKTDLVDLTLSTSGFIKGEKLQNYINRKVGGRQIQQFPIKFAAVATDFETGKAVAFNQG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNWLKLFKFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICATDLYSGRALYLSEG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.1%; Score 268.5; DB 2; 29.4%; Pred. No. 1.3e-15; tive 48; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 395;
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                                                                                                                                      A; Experimental source: strain C; Genetics:
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                                                                                                                                                                         A;Cross-references: GB:BA000007; PIDN:BAB35159.1; PID:g13361201; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-314 <H
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R;Hayashi, T.; Makino, gasawara, N.; Yasunaga, DNA Res. 8, 11-22, 2001
                        A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: H90845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: C; Genetics:
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: G85703
C;Accession: G85703
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-200:
C;Accession: G85703
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A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein ychK [imported] - C;Species: Escherichia coli
A;Status: preliminary
                                                                                                                                                                                                                                                      hypothetical protein ECs1736 [imported]
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                                                                                                                                                                             Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-200: Accession: H90845
                                                                                                                                                                                                                                Species: Escherichia col
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                                                                                                                                                                                                                                                                                                                                                                                     298 AVEKKMDE 305
                                                                                                                       T.; Makino, K.; Ohnishi,
N.; Yasunaga, T.; Kuhara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATDLYSGRALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLFVEPFQESGI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVTAPTATEIMTTSIQVLENRLKKNRMAGDPPDILIQPVCPQISTLDFHRAHAAIAAGQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRKI-KIGLALGSGAARGWSHIGVINALKKVGIEIDIVAGCSIGSLVGAAYAC-----DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATNISTGRELWFTEGDIHLAIRASCSIPGLMAPVAHNGYWLVDGAVVNPIPISLTRALGA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----FLAVRSNSEKRKEFC----DLVIVPELEEFTPLDVRKADQIMERGYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 258.5; DB 2;
Pred. No. 7.3e-15;
                                                                                                                         M.; Kurokawa, K.; Ishii
S.; Shiba, T.; Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli (strain
                                                                                                                                                                                                                                                        ŧ
                                                                                                                                                                                                                                                   Escherichia coli (strain 0157:H7, substrain
                                                                                                                                               K.; Ishii, K.; Yokoyama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                         M.; Shinagawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75;
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Potamousis,
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                                                                           coli 0157:H7
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K.; Apod
                                                                           and
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20.3%;

Score 258.5; DB 2; Pred. No. 7.3e-15;

Length

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C;Accession: AH0649
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Tiele: Complete genome sequence of a multiple drug resistant Salmonella enterica serow A;Accession: AH0649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein STY1296 [imported] - Salmonella enterica subsp. enterica (Sispecies: Salmonella enterica subsp. enterica esrovar Typhi A;Note: this species has also been called Salmonella typhi (C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: DNA
A,Realduss: 1-301 <PRX>
A)Cross-references: GB:AL513382; PIDN:CAD08379.1; PID:g16502423; GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 ATDLYSGRALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEFFQESGI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LAVRSNSEKRKEFC----DLVIVPELEBFTPLDVRKADQIMBRGYIKALEVLSE 251
                                                                                                                                                          186 DIVIA------VDLQHDAHLMQQDLLSFNVSEENSENGDSLPWHARLKERLGSITTRR 237
                                                                                                                                                                                                                                                                                                                                                                                                  --------FLAVRSNSEKRKEFC----DLVIVPELEEFTPLDVRKADQIMERGYI 243
                                                                                                                                                                                                                                                                                                                                                                                                                            238 AVTAPTATEIMTTSIQVLENREKRNRMAGDPPDILIQPVCPQISTLDFHRAHAAIÅAGQL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 PSLLKRVIWLKLFKFKPPLK-----GLIGWEKAIRFLEEVLPYRRIEKLEIPTYIC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 PTV------ CVDVLPIEPEKDIKNILHILLRSFP----- 201
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                                                                                                                             63 FSLLKRYNWLKLFKFKPPLK------GLIGWEKAIRFLEEVLPYRRIEKLEIPTYIC 113
                                                                                                                                                                                                                     114 ATDLYSGRALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEPFQESGI 173
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                                             3 LRKFEEINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 301;
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Pred. No. 8.4e-15;
9; Mismatches 113; Indels
49; Mismatches 106; Indels
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26.3%;
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Best Local Similarity 26.34
Matches 79; Conservative
78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 KALEVLSE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
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A;Gene: STX1296
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Search completed: June 19, 2003, 15:04:47 Job time : 29 secs

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Post-processing: Minimum Match 0%
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Perfect score:
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Maximum DB
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                      SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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SIDS2/gcgdata/geneseq/geneseqp-emb.
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Result No.	Score	% Query Match	% Query Match Length DB	DB	ID	Description
1	1273	100.0	251	18	AAW23071	Aquifex pyrophilus
2	913.5	71.8	249	18	AAW23074	Aquifex esterase V
ω	269.5	21.2	300	20	AAY38779	Neisseria meningit
	268.5	21.1	300	20	AAY38778	Neisseria meningit
ű	259.5	20.4	300	20	AAY38780	Neisseria gonorrho
9	223.5	17.6	1327	21	AAY70474	Human cyclic nucle
7	217.5	17.1	1389	22	ABB58963	Drosophila melanog
8	188.5	14.8	259	18	AAW23079	Whale mat sample 1
9	186	14.6	1402	22	ABG22116	Novel human diagno
10	168	13.2	283	23	ABP28552	Streptococcus poly

Arabidopsis thalia	AAG61569	21	384	6.6	84.5	5
Human polypeptide	AAM38969	22	558	6.7	85.5	44
Human polypeptide	AAM39046	22	546	6.7	85.5	43
DNA polymerase III	ABB84776	23	1161	6.8	86	42
	AAY51666	21	1161	6.8	86	41
	AAY52037	21	1161		86	40
	ABB54054	23	288	•	86.5	39
	AAG30646	21	414	6.8	87	38
Arabidopsis thalia	AAG30647	21	404	٠	87	37
Novel human diagno	ABG22113	22	838		88	36
Lactococcus lactis	ABB54471	23	349	6.9	88	35
O	AAW26740	18	388		88.5	34
Arabidopsis thalia	AAG38046	21	373	7.0	88.5	ω ω
	AAG38047	21	367	7.0	88.5	32
	AAG38048	21	361	7.0	88.5	31
-	ABB05483	23	885	7.0	89.5	
	AAG21350	21	376	7.0	89.5	29
	AAG21351	21	367	7.0	89.5	28
_	AAG21352	21	361	7.0	89.5	27
~	ABB91378	23	492	7.4	94.5	26
~	AAG38927	21	484	•	96.5	25
Arabidopsis thalia	AAG38928	21	381	7.6	96.5	24
Arabidopsis thalia	AAG38929	21	376	7.6	96.5	23
Novel human diagno	ABG22110	22	341	7.6	96.5	22
Drosophila melanog	ABB61634	22	480	8.4	107	21
Fat cell different	AAW86149	20	543	8.4	107.5	20
DNA encoding human	AAB70159	22	504	8.6	109.5	19
A bone marrow secr	AAY53641	21	504	8.6	109.5	18
Drosophila melanog	ABB71378	22	507	9.3	118	17
Propionibacterium	AAU61400	22	501		120	16
Human protein sequ	545	22	282	10.7	136	15
Streptococcus poly	ABP30534	23	269	11.2	142	14
	AAY38777	20	149	11.4	145	13
\sim	ABB52902	22	356	11.5	146	12
Streptococcus poly	ABP29892	23	283	13.2	168	11

ALIGNMENTS

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RESULT 1
AAW23071
ID AAW2
XX
AC AAW2
XX
AC AAW2
XX
AC 17-F
XX
                                                                                                                                                            BXXXXXX
Esterase; thermostable enzyme; ester; chiral compound; cheese; pulp; paper; lignin removal; sugar; lignocellulose; disease resistance; feedstuff.
        Callen W, Kosmotka A, Link S, Maffia AM, Murphy D; Reid J, Robertson DE, Swanson RV, Warren PV;
                                                                                                                                                                                                                                                                                                17-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                       AAW23071;
                                                                                                                                                                                                                                                                                                                                              AAW23071 standard; Protein; 251 AA.
                                                                 16-FEB-1996;
                                                                                       11-FEB-1997;
                                                                                                                                     WO9730160-A1
                                                                                                                                                                   Key Location/Qualifiers Misc-difference 248
                                                                                                                                                                                                      Aquifex pyrophilus strain KO1 5a.
                                                                                                                                                                                                                                                                           Aquifex pyrophilus esterase 28LC.
                                                                                                              21-AUG-1997
                                           (RECO-) RECOMBINANT BIOCATALYSIS INC.
                                                                 96US-0602359
                                                                                        97WO-US02039.
                                                                                                                                                           /note= "encoded by TGA"
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/note= "encoded by TAA"

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11-FEB-1997;
                          WO9730160-A1
                                                                                                     16-FEB-1996;
                                                                                                                                                      Callen W,
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ID AAY3
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                                                                                                                       pyrophilus, a Gram-negative, strictly chemolithoautotrophic Anality of pyrophilus, a Gram-negative, strictly chemolithoautotrophic Anality of as marine bacterium which grows optimally at 85 deg C and pH 6.8. Newly identified polynucleotides (AAT79321-30) encoding claimed esterases (AAW23069-77, AAW23089) were recovered from genomic gene cargines in host cells, and as probes to identify related sequences. The setrases are stable at high temperature and in organic rompounds used in pharaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group from an amino acid to an alpha-keto acid using scatters in carbohydrate in lighin removal in paper and pulp manufacture, in carbohydrate derivative synthesis, in fermentable sugar production from lighnocellulosic waste, in the study of plant wall tructure, plant resistance to disease and organic and the resistance to disease and organic matter decomposition and to select plants bred for production of highly degradable animal feeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GMFSLIKE:VNWLKLFKFKFKPPLKGLIGWEKAIRFLEEVLDFYRRIEKLEIPTYICATDLYSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 RALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEPFQESGIPTVCVDV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LRLRKFERINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 LPIEPEKDIKNILHILLRSFFLAVRSNSEKRKEFCDLVIVPELEEFTPLDVRKADOIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LRLRKFEBINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVPYASGYSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GMPSLLKRVNWLKLFKFKPPLKGLIGWEKAIRPLEEVLPYRRIEKLEIPTYICATDLYSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPIEPEKDIKNILHILLRSFFLAVRSNSEKRKEFCDLVIVPELEEFTPLDVRKADQIMER
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                 Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese or paper manufacture, and to study plant resistance to disease
                                                                                                               This protein comprises the thermostable esterase 28LC of Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baterase; thermostable enzyme; ester; chiral compound; cheese;
pulp; paper; lignin removal; sugar; lignocellulose;
disease resistance; feedstuff.
                                                                                                                                                                                                                                                                                                                                                                                         Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1273; DB 18;
100.0%; Pred. No. 9.8e-133;
ive 0; Mismatches 0;
                                                                                      Claim 19; Page 56-57; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW23074 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aquifex esterase VF5-34LC
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GYIKALEVLSE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aquifex sp. strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GYIKALEVLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 99
                                                                                                                                                                                                                                                                                                                                                               251 AA;
           N-PSDB; AAT79324
                                                                                                                                                                                                                                                                                                                                                                Sequence
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Addition to marrine strictly chemolithoautotrophic knall
gas bacterium that grows optimally at 85 deg C and pH 6.8

Newly identified polynucleotides (AAT7921-30) encoding claimed
sterases (AAW23069-77, AAW23089) were recovered from genomic libraries.

They can be used for recombinant production of the enzymes in host
cells, and as probes to identify related sequences. The esterases
are stable at high temperature and in organic solvents, making them
superior for use in production of pure chiral compounds used in
pharmaceutical, agricultural and other chemical industries. A
method is claimed for transferring an amino group from an amino
acid to an alpha-keto acid using a claimed esterase. The enzymes
cmay also be useful as ripening stearters in cheese making, in lignin
removal in paper and pulp manufacture, in carbohydrate derivative
synthesis, in fermentable sugar production from lignocellulosic
waste, in the study of plant wall structure, plant resistance to
disease and organic matter decomposition and to select plants bred
for production of highly degradable animal feeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEPFQESGIPTVCVDV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPIEPEKDIKNILHILLRSFFLAVRSNSEKRKEFCDLVIVPELEEFTPLDVRKADQIMER 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 LPITQERKIKULHILIRSFFLAVRSNSEKRKEFCNVVIEPPLEERSPLDVNKADBIF-C 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 EMLKLLKEVNWLKLFKFKTPKMGLMGWEKAABFLEKELGVKRLEDLNIPTYLCSADLYTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LRLRKFEEINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese or paper manufacture, and to study plant resistance to disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.8%; Score 913.5; DB 18; Length 249; 72.0%; Pred. No. 8.5e-93; ive 31; Mismatches 37; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein comprises the thermostable esterase VF5-23LC of
                                                                                                                                                                                                                                 Murphy D;
                                                                                                                                                                                                                            Link S, Maffia AM, Mi
Swanson RV, Warren PV;
                                                                                                                                             (RECO-) RECOMBINANT BIOCATALYSIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 19; Page 59-60; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY38779 standard; Protein; 300 AA.
97WO-US02039
                                                                           96US-0602359
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Matches 177; Conservative
                                                                                                                                                                                                                            , Kosmotka A,
Robertson DE,
                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-425035/39.
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GDMRAL 249
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RESULT 4
AAY38778
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Best Local S
Matches 70
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10-DEC-1997;
14-JAN-1998;
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06-NOV-1997;
14-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis and N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (ORFs) AAZ11972-Z12358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria
                                                                                                                                                                                                                                                                                                                                        infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grandi
                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 324; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteins from Neisseria meningitidis and N. gonorrhoeae useful for diagnosis, treatment and prevention of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
treatment; Neisseria infection; meningitis; septicaemia; gonorrhea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis strain A antigen encoded by ORF137.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-1997;
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                                                                                                                166
                                                                                                                                      129
                                                                                                                                                               106 LGKTDLVDLTLSTSGFIKGEKLQNYINRKVGGRRIQQFPIKFAAVATDFETGKAVAFNQG
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                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                              INLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGMFSLLKR
                                                                                                                NAGQÁVRASAÁÍ PNVFQÞVI I GRHTYVÐGGLSQÞVÞVSAARRXXXXXVI AVDI SARÞSKN
                                                                                                                                      SLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEPFQESGIPTVCVDVLPIEPEKD
                                                                                                                                                                                        VNWLKLFKFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICATDLYSGRALYLSEG
                                                                                                                                                                                                               VGLALGGGASKGFAHVGIIKVLKENGIPVKVVTGTSAGSIVGSLFASGMSPDRLELEAEI
                                                             IS----QGFFSYLDQTLNVMSVSALQNBLGQADVVIKPQV 261
                                                                                      IKNILHILLRSFF-----LAVRSNSEKRKEF--CDLVIVPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Masignani
                                                                                                                                                                                                                                                                                                                  300 AA;
                                                                                                                                                                                                                                                                   Conservative
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97GB-0026147.
98GB-0000759.
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97GB-0024386.
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97GB-0023516.
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                                                                                                                                                                                                                                                                  40;
                                                                                                                                                                                                                                                                Score 269.5; DB Pred. No. 3.9e-210; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rappuoli R,
                                                                                                                                                                                                                                                                                         DB 20;
                                                                                                                                                                                                                                                                  ; 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scarlato
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                                                                                                                                                                                                                                                                                        Length
                                                                                       223
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                                                                                                                                                                                                                                                                                         300;
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RESULT 5
AAY38780
ID AAY3
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AAY38778

standard; Protein;

300 AA

AAY38780

standard;

Protein; 300 AA

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Best Local
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06-NOV-1997;
14-NOV-1997;
                                                                                                                                                                                                                                                                      Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis and N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (ORFs) AAZ11972-Z12358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria n
treatment;
                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                              Proteins from Neisseria meningitidis and N. gonorrhoeae useful for diagnosis, treatment and prevention of infection {\bf r}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JAN-1998;
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226
                        189
                                                                                                  106 LGKTDLVDLTLSTSGFİKGEKLQNYINRKVGGRQİQQFPİKFAAVATDFETGKAVAFNQĞ
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                                                                                                                         69
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                                                                                                                                                                70;
                                                                                                                                                                                                             Similarity
                                                                  SLIPALLGSCAIPGIFEPVBYKNYLLVDGGIVNNLPVBPFQESGIPTVCVDVLPIBPBKD
                                                                                                                         VNWLKLFKFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICA!DLYSGRALYLSEG
                                                 NAGQÁVRASAÁ I PNV POP VI I GRHTY V DGGLSOP V PV SAARROGANF VI AVDISAR PGKN
                                                                                                                                                 VGLALGGGASKGFAHVGIIKVLKENGIPVKVVTGTSAGSIVGSLFASGMSPDRLELEAEI 105
IS-----QGFFSYLDQTLNVMSVSALQNELGQADVVIKPQV
                        IKNILHILLRSFF-----LAVRSNSEKRKEF--CDLVIVPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            meningitidis; Neisseria gonorrhoeae; antigen; vaccine; Neisseria infection; meningitis; septicaemia; gonorrhea
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                                                                                                                                                                                                  Conservative
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97GB-0025158.
97GB-0026147:
98GB-0000759.
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97GB-0023516.
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                                                                                                                                                                                                             21.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pizza
                                                                                                                                                                                                 ; Score 268.5; DB 2; Pred. No. 5.1e-21; 41; Mismatches 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoded by ORF137.
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                        223
                                                                                                                                                                                                                         300;
                                                                                                                                                                                                 15;
                                                                                                                                                                                                 Gaps
                                                                          188
                                                                                                  165
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                                                                                                                                                                          68
                                                   225
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us-09-903-410-36.rag

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Cyclic nucleotide-associated protein-2; CNAP-2; human; cytostatic; anti-arteriosclerotic; hepatotropic; anti-leukaemic; anti-inflammatory; immunomodulatory; anti-asthmatic; anti-leukaemic; anti-inflammatory; anti-asthmatic; anti-antemic; anti-epileptic; diagnosis; anti-Alzheimer's; anti-Parkinsonian; cerebroprotective; ophthalmological; anti-Alzheimer's; anti-Parkinsonian; cerebroprotective; ophthalmological; anti-infertility; anti-Allergic; vasotropic; immunosuppressive; hypotensive; gene therapy; prevention; treatment; arteriosclerosis; cell proliferative disorder; autoimmune/inflammatory; diabetes mellitus; neurological; vision; reproductive; smooth muscle.
                                                                                                                                                                                                                                                                                                                                                                        35.1327
/label= Mature_CNAP-2
/note= "Shares 24% identity to Aquifex pyrophilus
esterase 28LC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Potential phosphorylation site"
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                                                                                Human cyclic nucleotide-associated protein-2 (CNAP-2).
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|abel= Signal_peptide
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                                                 (first entry)
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                                               04-JUL-2000
                                                                                                                                                                                                                                                                                        Homo sapiens
              AAY70474;
                                                                                                                                                                                                                                                                                                                                      Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis and N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (NFE) AAZ11972-Z12358. The antigenic proteins, their fragments, their mucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 INLVLSGCAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGMFSLLKR
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                                                                                                             Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
treatment; Neisseria infection; meningitis; septicaemia; gonorrhea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scarlato V;
                                                                                Neisseria gonorrhoeae antigenic protein encoded by ORF137.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 325; 524pp; English.
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97GB-0024190.
97GB-0024386.
97GB-0025158.
97GB-0026147.
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Best Local Similarity 31.4%
Local Similarity 31.4%
To 70; Conservative
                                             (first entry)
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                                                                                                                                                                  Neisseria gonorrhoeae
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            AAY38780
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/note= "Potential phosphorylation site" 1301

Modified-site Modified-site

AAY70474 standard; Protein; 1327 AA.

RESULT 6 AAY70474 ID AAY

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The present sequence is a human cyclic nucleotide-
associated protein-2 (CNAP-2), identified in Incyte clone 3149674,
that is isolated from ADRENON04 cDNA library. It is expressed in
nervous, reproductive, cardiovascular and hammatopoietic/immune tissues.
                                                                                Isolated cyclic nucleotide associated proteins useful for preventing, diagnosing and treating cell proliferative, autoimmune/inflammatory, neurological, vision, reproductive and smooth muscle disorders -
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                                                                Disclosure; Page 64-67; 78pp; English.
                                                                                                                        N-PSDB;
                                                                                                                                                  Hillman JL,
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Best Local S
Matches 74
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              New isolated nucleic acid genes from Drosophila and
                                         N-PSDB;
                                                                                                                                                                                Drosophila melanogaster
                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ
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                                                                                                    23-MAR-2000;
11-JUL-2000;
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                                                                  Adams M,
                                                                                                    2000US-191637P
2000US-0614150
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                                                                   PWD,
             detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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67 KR----VNWLKLFKFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICATDLYSG-- 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 EEINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGMFSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 ENSSLVLSGGGALGIAHLGVLHDLEKONIVPNEIVGTSMGGIIGASMAIGMKEKEILEEI
                                                                                                      This protein comprises the whale mat sample 11.801 esterase es9. Newly identified polynucleotides (ART79321-40) encoding esterases (AM23069-88), some of which are claimed, can be used for recombinant production of the enzymes in host cells. The esterases are stable at high temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group from an amino acid to an alpha-keto acid using a claimed esterase. The enzymes may
                        or
                                                                                                                                                                                                                                                                  also be useful as riportaing starters in cheese making, in light removal in paper and pulp manufacture, in carbohydrate derivative synthesis, in fermentable sugar production from lignocellulosic waste, in the study of plant wall structure, plant resistance to disease and organic matter decomposition and to select plants bred for production of highly degradable animal feeds.
   Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese paper manufacture, and to study plant resistance to disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                14.8%; Score 188.5; DB 18; Length 27.3%; Pred. No. 3.2e-12; Live 43; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy;
food supplement; medical imaging; diagnostic; genetic d
                                                                        Disclosure; Page 64-65; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #22107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG22116 standard; Protein; 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 LDVRKADQIMERG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 FQFHKHKEIRALG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 69; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                259 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG22116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 970 KAREWSKKMTKWPLQLLDLTYPITSMFSGREFNKTIHDTFGDVSIEDLWIPYFTLTTDIT 1029
                                                         18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 SGRALYLSEGSLIPALLGSCAIPGIFEPV--EYKNYLLVDGGIVNNLPVEPFQESGIP-T 175
                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                             9 INLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGMFSLL--
                                                                                                                                                                                                                                                                                                                                                                                                                              -----KRVNW-LKLFKFFPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICATDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1090 IAIDVGSQDDTDLTNYGDDLSGWWLLYKKWNPFTSPVKVPDLPDIQSRL-----AYVSCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 VCVDV------LPIEPEKDIKNILHILLRSFFLAV
                                                                                                                                                                                                                                                                                     DB 22; Length 1389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e; ester; chiral compound; cheese; sugar; lignocellulose;
SEQ ID NO 3681; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                     discloses genomic DNA sequences (ABL16176-ABL3051I), esequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murphy D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSNSE-KRKEFCDLVIVPELEEFTPLDVRKADQIMERGYI 243
                                                                                                                                                                                                                                                                                  17.1%; Score 217.5; DB 22; larity 26.1%; Pred. No. 2.2e-14; Conservative 44; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maffia AM, M
V, Warren PV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Esterase; thermostable enzyme; ester;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whale mat sample 11.801 esterase es9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RECO-) RECOMBINANT BIOCATALYSIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Link S, Ma
Swanson RV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW23079 standard; Protein; 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pulp; paper; lignin removal; s
disease resistance; feedstuff.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0602359.
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Reid J, Robertson DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-425035/39.
N-PSDB; AAT79332.
                                                                                                                                                                                                                                                 1389 AA;
                                                                                                                                                          (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                   Local Similarity
tes 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-PEB-1997;
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Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
               Streptococcus polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID No 52475; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT, Liu C,
                                                              02-JUL-2002
                                                                                                        ABP28552
                                                                                                                                                ABP28552 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1025 RTKQRAREWAKSMTSVLEPV-----LDLTDPATSMFTGSAFNRSIHRVFPGXSRFEDLFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                    QFPPGPNVSCVRQLEVVKSSSYCE-YLRPPIDCFKTMDFGKFDQIYDVGY 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTRGNTIALVLGEGAHGARGCSHIGVLKALEBAGVPVDLVGGTSIGSFIGALYAEERSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRKFBEINLVLSGGA--AKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVPYASGYS--
                                                                                                                                                                                                                                                                                                                                     LPADIARSMGAKTVIAIDVGSQDETDLSTYGDSLFGWWLLWKRLNPWGLTRXRFPDMAEI
                                                                                                                                                                                                                                                                                                                                                                        LPVBPFQESGIPTVCVDVLPIBPEKDIKNILHILLRSFFLAVRSNS---------
                                                                                                                                                                                                                                                                                                                                                                                                                     PYFKRXPTD1TASAMRGHKDGSLWRYVRASMDTLSGYLPPLCDPKD--GHLLMDGGY1NN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTY-ICATDLYSGRALYLSEGSL---IPALLGSCA--IPGIFEPVEYKNYLLVDGGIVNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----PEGMFSLLKRVNWLKLFKFKPPLKGLIGWEKAIRFLEEVLP-YRRIEKLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1402 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                            (first entry)
                                                                                                                                                Protein; 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.6%;
                                                                                                                                                                                                                                                                                          EKRKEFCDLVIVPELEEFTPLDVRKADQIMERGY 242
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Pred. No. 7.1e-11;
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                        6280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1402;
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                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a protein (ABP25413-ABP30895) from group B CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus yvogenes), comprising one of 5483 sequences (S1), given in CC the specification. The proteins have antibacterial and antiinflammatory CC activity. (I), mucleic acids encoding (I), ABN66044-ABN71826 and CC antibactes that bind (I) are used in the manufacture of medicaments for CC the treatment or prevention of infection or disease caused by CC Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. CC Mucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by CC acid encoding (I) may be used to treated may be meningitis. Nucleic CC acid encoding (I) may be used to recombinantly produce (I) and may be CC used in gene therapy. Antibodies to (I) are used for affinity immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-2000;
24-NOV-2000;
07-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
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                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus proteins.
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Tettelin H;
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DB; ABN69183.
179
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INST GENOMIC RES
                                                                        MTSGKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKXYLDGGLSDSIPVDEARGLGF
                                                                                                           LYSGRALYLSEGSL---IPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEPFQESGI
                                                                                                                                                                                                                                                              INLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGMFSLLKR
DKLIVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDL
                                -PTVCVDVLPIEPEKDIKN--ILHILLRSFFLAVRSNSEKRKEFCD-LVIVPELEEFTPL
                                                                                                                                                 YN--KKYLSHPKYMSLRSWFRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATE
                                                                                                                                                                                   VGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERAL-----R
                                                                                                                                                                                                                                                                                                                                                                             283 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2000GB-0026333.
; 2000GB-0028727.
; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                   13.2%; Score 168; DB 23; 23.7%; Pred. No. 6.8e-10;
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                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                       Length 283;
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                                                                                                                                                                                                                                                                                      179 DKLIVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKYMSLEKTGDL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a library of DNA fragments of Escherichia coli strains comprising polynuclectides (DABBS77-ABBS923) and ABBS9533) and encoded proteins (ABBS2459-ABBS2919 and ABBS2954-ABBS3094) of nature B2/D-A-. The polynuclectides have potential antiinflammatory, antibacterial and immunosuppressive activity as part of pharmaceutical compositions used to treat, palliate or prevent extra-intestinal E. coli infections. The polypeptides are useful for determining the phylogenic group of a given E. coli strain. These polypeptides can detect and treat an undesired development of E. coli, particularly an extra-intestinal infection that include systemic and non-diarrhoeal infections such as septicaemia, pyslonephitis and meningitis this is particularly advantageous as bacterial resistance is increasing with the more frequent use of broad spectrum antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A library of DNA fragments of Escherichia coli strains for the phylogenic determination of a given strain comprises polynucleotides of nature 82/D+A-
                                                                                                            117 LYSGRALYLSEGSL---IPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEPFQESGI
                                                                                                                                                   174 -PIVCVDVLPIEPEKDIKN--ILHILLRSFFLAVRSNSEKRKEFCD-LVIVPELBEFTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli; B2/D+A-; antiinflammatory; antibacterial; immunosuppressive; extra-inteetinal infection; phylogeny; meningitis; systemic infection; non-diarrhoeal infection; septicaemia; pyelonephritis; antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                               230 ------DVRKADQIMERGYIKALEVLSE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 FAIRPSKSLVIGRLEKNPDKLDSİYQLGMKDAKSVMPE 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%; Score 146; DB 22; 24.4%; Pred. No. 2.6e-07; iive 40; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonacorsi S, Clermont O, Nassif X,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli polypeptide SEQ ID NO 1215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB52902 standard; Protein; 356 AA.
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02-FEB-2001; 2001FR-0001449.
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Best Local Similarity 24.4
Matches 87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 VNWLKLFK!?KPPLKGLIGWEKAIRFLEEVLPYRRI-------BKLEIPTYICATD 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grandi G,
   239 FAIRPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPE 276
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                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus polypeptide SEQ ID NO 8960
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                                                                                                                                                                          ABP29892 standard; Protein; 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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                                                                                                                                                                                                                                                                                                                         (first entry)
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(GENO-) INST GENOMIC RES.
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66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus agalactiae.
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N-PSDB; ABN70523.
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                                                                                                                                                                                                                                                                                                                     02-JUL-2002
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06-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine; treatment; Neisseria infection; meningitis; septicaemia; gonorrh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis antigen encoded by a partial ORF137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-1999
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                       and N. gonorrhoeae antigenic proteins. They are encoded by open
reading frames (ORFS) AAZ11972-Z12358. The antigenic proteins,
their fragments, their nucleic acids and antibodies are used for
diagnosis, prevention (as vaccines) or treatment of Neisseria
                                                                                                                                                                                     Claim 4; Page 322; 524pp; English.
                                                                                                                                                                                                                                                                                                                              WPI; 1999-327407/27.
N-PSDB; AAZ12212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-NOV-1997,
10-DEC-1997,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAY-1999
                                                                                                                                                                                                                                           Proteins from Neisseria meningitidis and N. gonorrhoeae useful for diagnosis, treatment and prevention of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-NOV-1997;
18-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237
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                                                                                                                                   acid sequences AAY38499-Y38944 represent Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLA-HTDAWRQQGYEDTMLTME-----HIRKPLAARQVLSRSETVLQKSLEITEE 343
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97GB-0024190.
97GB-0024386.
97GB-0024386.
97GB-0025158.
97GB-0026147.
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                                                                                                                                      meningitidis
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                     CC The invention relates to a protein (ABP25413-ABP30895) from group B CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus youngers), comprising one of 5483 sequences (31), given in CC the specification. The proteins have antibacterial and antiinflammatory CC activity. (1), nucleic acids encoding (1) ABN66044-ABN71526 and CC antibodies that bind (1) are used in the manufacture of medicaments for CC the treatment or prevention of infection or disease caused by CC Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. CC Nucleic acids encoding (1) are used to detect Streptococcus in a bind to CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be used as a vaccine or diagnostic composition. The disease caused by CC Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity aronacon and antipolarian and may be correctly and may be used for affinity and may be moreains.
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                                                                                                                                                                                                                                                                                                                                                                 New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-OCT-2000; 2000GB-0026333
24-NOV-2000; 2000GB-0028727
07-MAR-2001; 2001GB-0005640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus polypeptide SEQ ID
                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 4155; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Telford J,
Tettelin H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-352536/38
DB; ABN71165.
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INST GE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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               proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269
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Pred. No. 9.5e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser C;
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completed: June 19, 2003, 15:02:22
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antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
antibacterial; endocrine; cardiant; central nervous system; virucide;
w antispregant; antimutegen; cardiavascular; antianaemic; anaemia;
antisgregant; haemostatic; vulnersary; antiulcer; osteopathic; eczema;
w dermatological; antiallergic; antiastmatic; antidiabetic; cytostatic;
w meuroprotective; antidepressant; nootropic; antidiabetic; cytostatic;
w meuroprotective; antidepressant; nootropic; antidiabetic; cytostatic;
w mitianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
w antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
w cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
genetic disease; haematopoietic disorder; platelet disorder; asthma;
thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
w allergic rhinitus; diabetes; multiple sclerosis; depression;
w allergic rhinitus; diabetes; multiple sclerosis; depression;
w allergic specific disease; neurodegenerative disorder;
                                                          ω
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                                                                                                                                                PPLKGLIGWEKAIRFLEEVLPYRRI------EKLEIPTYICATDLYSGRALYLS 126
                                                                                                                                                                  127 BGSL---IPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEPFQESGI-PTVCVDVLP 182
                                                                                                                                                                                                                            19 KGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGMPSLLKRVNWLKLFKFK 78
                                                                                                                 54
                                                                                                       2 RGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERAL----RYN--KKYLSH
                                                                                                                                                                                                                                                                   183 IEPEKDIKN--ILHILLRSFFLAVRSNSEKRKEFCD-LVIVPELEEFTPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated human polynucleotides encoding polypeptides, useful for the
                                                          Gaps
                                                          42;
                           ch 11.2%; Score 142; DB 23; Length 269; Similarity 22.8%; Pred. No. 4.9e-07; 61; Conservative 51; Mismatches 114; Indels 4
                                                                                                                                                                                                                                                                                                                                                         235 IGRLEKNPDKLDSIYQLGMKDAKSVMPE 262
                                                                                                                                                                                                                                                                                                                              -----DVRKADQIMERGYIKALEVLSE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein sequence SEQ ID NO:971.
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM25456 standard; Protein; 282 AA
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                           Query Match
Best Local Similarity
Matches 61; Conserv
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269 AA;
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Sequence
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AMM25025 to AAM99904 encode the human proteins given in AAM25225 to AAM2503. The proteins can have activities based on the tissues and cells they are expressed in, such as: antinflammatory, antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrime; cardiant; cardiavascular; antianemic; antiapacental; endocrime; cardiant; cardiavascular; antianemic; antiagram; haemostatic; vulnerary; antidateric; osteopathic; darmatological; antialteric; unlnerary; antidateric; oytostatic; neuroprotective; antidepressant; nootropic; antidateric; cytostatic; neuroprotective; antidepressant; nootropic; antidateric; oytostatic; neuroprotective; antidepressant; nootropic; antidateric; oytostatic; neuroprotective; antidepressant; nootropic; conciding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polymucleotides are useful for screening for agondtis or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, renumented arthritis, septic shock, panoreatitis, cardiac dysfunction, infections, autoimmunity, genetic diseases, haematopoietic disorders, and infections, understant and insured the infections, understant and insured the antipoletic disorders, and infections, understant and insured the antipoletic disorders, and infections, understant and insured the antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and antipoletic disorders, and anti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 GRALYLSEGSLIPALLGSCAIPGIFEPV--EYKNYLLVDGGIVNNLPVEPPQESGIPTV- 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoprosis, severe combined immunodeficienty, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and
treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.7%; Score 136; DB 22; Length 282; 23.0%; Pred. No. 2.4e-06; tive 37; Mismatches 91; Indels 36
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                                                                                                                                   20; Page 205; 1217pp; English.
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Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurological disorders.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein search, using sw model
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Copyright (c) 1993 - 2003 Compus
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Sequence 39, Appl
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US-08-602-359A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOSTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,359A
FILING DATE: February 16, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5090
TELEPAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 AMINO ACIDS
                                                                TYPE: AMINO TOPOLOGY: LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SWANSON,
APPLICANT: WARREN, I
APPLICANT: KOSMOTKA,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: "44".
STREET: "44".
CITY: LA JOLLA
CTATE: CALIFORNIA
TISA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                        AMINO ACID
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5942430
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SWANSON, Ronald V.
WARREN, Patrick V.
KOSMOTKA, Anna
INVENTION: ESTERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4225 EXECUTIVE SQUARE, STE 1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REID, Jo
MAFFIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROBERTSON, Daniel E.
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  99.48;
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  Score 1265;
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  DB
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Length 251;
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Sequence 55, Appl
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Result No.

Query Match

Length

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74 74

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Issued_Patents_AA:*

Sequence: Title: Perfect score:

US-09-903-410-36 1273

OM protein

Scoring table:

BLOSUM62

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                                                                                                                                                            STATE: Virginia
COMPUTE: Virginia
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATE:
PLING DATE: 15-Jul-1999
CLASSIFICATION: 15-31-1999
CLASSIFICATION: 15-31-1999
CLASSIFICATION: 15-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-31-16-3
                                                                                                                          1 IRLRKFERINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dixon, Mark S
Jones, David A
Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes and uses
               Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 6287865th Glebe Road
                                                                     Indels
         70.8%; Score 901.5; DB 2; 71.5%; Pred, No. 2.1e-94; ive 31; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-0CT-1997
APPLICATION NUMBER: PCT/GB96/00795
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ms Mary J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 627
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09353585
Patent No. 6287865
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
         Query Match
Best Local Similarity 71.54
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ::||
244 GDMRAL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GYIKAL 246
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                                                                                                                                                                                                        61 GMPSLLIRRVNWLKLFKFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLRIPTYICATOLYSG 120
                                                                                                                                                                                                                                        61 GMFSLLKRVNWLKLFKFKPPLKGLIGWEKAIRPLEEVLPYRRIEKLEIPTYICATDLYSG 120
                                                                                                                                                                                                                                                                                                                      RALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLFVEFFQESGIPTVCVDV 180
                                                                                                                                                                                                                                                                                                                                                            181 LPIEPEKDIKNILHILLERSFFLAVRSNSEKRKEFCDLVIVPELEEFTPLDVRKADQIMER 240
                                                                                                                                                                                                                                                                                                                                                                                                                                       LPIEPEKDIKNILHILLRSFFLAVRSNSEKRKEFCDLVIVPELEEFTPLDVRKADQIMER 240
                                                                                                                          1 LRLRKFIBEINLVLSGGAAKGIAHIGVIKAINELEIRVRALSGVSAGAIVSVFYASGYSPE 60
                                                                                       LRLRKFEBINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPE
                                        Gaps
                                        ö
                                  Indels
      Pred. No. 9.4e-136;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 4225 EXECUTIVE SQUARE, STE 1400 CITY: LA JOLLA STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTMARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,359A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09010/01060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MURPHY, Dennis
APPLICANT: REID, John
APPLICANT: MAFFIA, Anthony
APPLICANT: SWANSON, Steven
APPLICANT: SWANSON, Patrick V.
APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  February 16, 1996
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HALIE, LISA A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROBERTSON, Daniel E. MURPHY, Dennis REID, John
Best Local Similarity 99.6%; Pr
Matches 250; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GYIKALEVLSE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GYIKALEVLSE 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LINEAR
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CLASSIFICATION:
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US-09-353-585-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09353585
Patent No. 6287865
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                       TELEFAX: (703) 816-4
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

NEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOPTWARE: PAtentin Release #1.0, Version

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Lixon & Vanderhye PC
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 6287865th Glebe Road
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-0CT-1997
APPLICATION UNMBER: PCT/GB96/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               NAME: MS MATY J WILSON
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Plant pathogen resistance genes and uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dixon, Mark S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             607 YNNOLSGSIPEEI-GYLSSLTYLSL--GNNSLNGLIPASFANMRNLQALILNDNNLIGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     664 PSSVC--NLTSLEVLYMPRNNLKGKVPQCLGN 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 PTYICATDLYSGRALYLSEGSL---IPALLGS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        550 LNNLSRLNLVNNQLSGSIPE---EIGYLRSLNDLGLSENALNGSIPASLGNLNNLSMLYL 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 ----ASGYSPEGMESILIKRVNWIKIFKEKPPIKGJIGWBKA-IRFIBEVIPYRRIEKIBI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 6.8%; Score 86.5; DB 4; Length 1112;
1 Similarity 30.3%; Pred. No. 1.2;
46; Conservative 25; Mismatches 56; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LRKFEEINLV---LSGGAAKGIAHIGVLKAINELGIRVRALSG---VSAGAI--VSVFY- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE: 15-Jul-1999
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
1/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/353,585 FILING DATE: 15-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Arlington
STATE: Virginia
                      TYPE: amino acid
STRANDEDNESS: <U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America ZIP: 22201-4714
                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Tomato
                                                                   ENGTH: 1112 amino acids
                                                                                                                                                           (703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jonathan DG
                                                                                                                                  816-4100
                                                                                                                                                                                                        620-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #1.25
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US-08-977-554-2
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                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: PASSESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,554
FILING DATE: US/08/977,554
CLASSIFICATION: 536
CLASSIFICATION DATA:
APPLICATION UNMBER: PCT/US97/02318
APPLICATION UNMBER: PCT/US97/02318
FILING DATE: 19-FEB-1997
ATTORNEY/ACENT INFORMATION:
NAME: Dickinson, 0. Todd
REGISTRATION NUMBER: 28,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFOR
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 393 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19103-2793
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ribA
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                  REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215/994-2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN: Cf2
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     550 LNNLSRLNLVNNQLSGSIPE---BIGYLRSLNDLGLSENALNGSIPASLGNLNNLSMLYL 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   651 ALILNDNNLIGEIPSSVC--NLTSLEVLYMPRNNLKGKVPQCLGN 693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             607 YNNQLSGSIPEEI-GYLSSLTYLSL--GNNSLNGLI---
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: 393 amino acids
amino acid
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                                                                                                              215/994-2222
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Black, Michael
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Traini, Christopher M.
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                                                                                                                                                                                  P50444-07
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132 PALLGSCAIPGIF------EPVEYKN-----YLLVDG---GIVNNLPVEPFQ 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 IRFLEEVLPYRR----IE---KLEIPTYICATDLYSGRALYLSEGSLI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 ESGIPTVCVDVLPIEPEKDIK------NILHILLRSFPLAVRSNSEKRKEFCDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91; Indels 75; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.4%; Score 81.5; DB 4; Length 393; Best Local Similarity 22.1%; Pred. No. 0.88; Matches 58; Conservative 39; Mismatches 91; Indels 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89BB: Dechert, Price & Rhoads
F: 4000 Bell Atlantic Tower, 1717 Arch Stre
Philadelphia
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER: PCT/US97/02318
FILING DATE: 19-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 VIVPELBEFTPLDVRKADQIMER 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 DIAERIEVIVPETVHNHDYMVTK 385
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/977,554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palmer, Leslie M.
Fedon, Jason C.
Warren, Richard L.
Traini, Christopher M.
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APPLICANT: Warren, Sichard L.
APPLICANT: Traini, Christopher M.
APPLICANT: Wang, Min
APPLICANT: Wooney, Jeffrey
APPLICANT: Bebouck, Christine
APPLICANT: Debouck, Christine
APPLICANT: Bachouck, Christine
APPLICANT: Black, Michael
TITLE OF INVENTION: ribA
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: Dechert, Frice & Rho
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Patent No. 6280971
GENERAL INFORMATION:
APPLICANT: Palmer, Leslie M. APPLICANT: Fedon, Jason C.
                                                                                INPORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERLESTICS: LENGTH: 393 amino acids: TYPE: amino acid STRANDENESS: single: TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
        TELEFAX: 215/994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                 32 BLGIRVRALSGVS-AGAIVSVFYASGYSPEGMPSLLKRVNWLKLFKFKPPLKGLIGWEKA 90
                                                                                                                                                                                                                                                     75; Gaps
                                                                                                                                                                Ouery Match 6.4%; Score 81.5; DB 2; Length 393; Best Local Similarity 22.1%; Pred. No. 0.88; Matches 58; Conservative 39; Mismatches 91; Indels 7:
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STREET: 4000 Hell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
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COUNTRY: USA
ZIP: 19103-2793
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compartible
COMPUTER: IBM Compartible
COMPUTER: IBM Compartible
COMPUTER: BacksEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,967
FILING DATE:
CLASSIPRICATION DATA:
PRIOR APPLICATION DATA:
ATPLICATION NUMBER: US/08/977,554
ATTLING DATE:
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JRAMATION:

F. Palmer, Leslie M.

AT: Fedon, Jason C.

ANT: Warren, Richard L.

LCANT: Warren, Richard L.

LICANT: Wang, Min

PILICANT: Wooney, Jeffrey

APPLICANT: Debouck, Christine
APPLICANT: Black, Michael

TILES OF INVENTION: Xib

NUMBER OF SECURNICAN: Xiba

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FILING DATE: 19-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, 0. Todd
REGISTRATION NUMBER: 28,354
REPRENCK/POCKEY NUMBER: P50444-07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215/994-2255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 DIAERIEVIVPETVHNHDYMVTK 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09225967; Patent No. 6171598; GENERAL INFORMATION:
             single
; STRANDEDNESS: sir
; TOPOLOGY: linear
US-08-977-554-2
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US-09-225-967-2
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US-07-977-434-12
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Best Local S
Matches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5466591 'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/07977434 Patent No. 5466591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/07/:
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 590
PRIOR APPLICATION NUMBER: US 590
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Dickinson, Q. Todd
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215/994-2252
                                                                                                                                                                             SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                       STATE: New Jersey
ZIP: 07110-1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                              OPERATING SYSTEM:
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                                      US 590,466
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 Sequence 12, Application US/08458819
Patent No. 5795762
GEMERAL INFORMATION:
APPLICANT: Gelfand, David H.
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US-07-977-434-12
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
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TOPOLOGY: linear
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REGISTRATION NUMBER: 31,822
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KLRRLLEDSKEDLOKSIELV---ELIYDVPMDVEK-DEIIYRGYNPDKLLKVLKK 278
                                                                                                                                                     GDKDLLQLVSDKVFVWRVER-----GITDL----VLY-DRNKVIEKY------GIY- 176
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                                                                           PEOFKDYLSLVGDQIDNIP-----GVKGIGKKTAVSLL--KKYNSLENVLKNINLLTE
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APPLICANT: Abramson, Richard D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 PVEYKNYLLVDGGIVNNLPVEPFQESGIPTV----CVDVLPIEPEKDIKNIL---HILLR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 VLKAINBLGIRVRALSGVSAGAIVSVFYASGYSPBGMFSLLKRVNWLKLFKFKPPLKGLI 95
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GENERAL INPORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSER: Cetus Corporation
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PRIOR APPLICATION DATE: 08 899,241
PRILOR DATE: 2-AUG-1986
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 746,121
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: 2.AUG-1991
PRIOR APPLICATION DATA: 2.AUG-1991
PRIOR APPLICATION NUMBER: WO PCT/US90/07641
PILING DATE: 21-DEC-1990
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MEDIUM TYBE: FLOPPY disk
COMPUTER: LBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordferfect 5.0
CURSENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07035
FILING DATE: 19910930
CLASSTEICATION DATA:
APPLICATION NUMBER: US 500,490
FILING DATE: 28-SEP-1990
FILING DATE: 28-SEP-1990
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,213
FILING DATE: 15-MAY-1990
PRIOR APPLICATION NUMBER: US 523,394
FILING DATE: 15-MAY-1990
PRIOR APPLICATION NUMBER: US 523,441
FILING DATE: 12-JAN-1988
PRIOR APPLICATION NUMBER: US 143,441
FILING DATE: 12-JAN-1988
PRIOR APPLICATION NUMBER: US 183,441
FILING DATE: 11-JAN-1988
FILING DATE: 11-JAN-1988
FILING DATE: 11-JAN-1987
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PCT-US91-07035-12
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Best Local Similarity
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APPLICANT:
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                                                                                  COMPUTER READABLE FORM
                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                 TILE OF INVENTION: DIAGNOSIS AND TREATMENT OF INVENTION: SAD RELATED DISORDERS
                                                                                                                                                                ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: Case No. 2580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 609,157 FILING DATE: 02-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 58
PILING DATE: 20-SEP-1990
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
                                                 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199 SFFLAVRSNSEKRKEFCDLVIVPELEEFTPLDVRKADQIMERGY--IKALEVLSB 251
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California
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David Markby
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415-420-3300
TD NO: 12:
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                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                              ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAVING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                  STREET:
                                                                                                                   COUNTRY:
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   APPLICATION DATA
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Query Match 6.1
Best Local Similarity 21.9
Matches 42; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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LENGTH: 488 amino acids
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FILING DATE: June 18, 19
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
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                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                         TITLE OF INVENTION:
                                                                                                          UMBER OF SEQUENCES:
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                                                    ADDRESSEE: W. MURRAY SPRUILL (ALSTON & BIRD, LLP) STREET: 3605 GLENWOOD AVE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 LPVEPFQESGIP 174
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                                RALEIGH
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MUNDELL, UNITED BRIAN
KA
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FALLIS, LYNN
MEYER, TERRY E
MUNDELL, SCOTT A
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USA
                                                                                                                                                                                                                                                                          CIGAN
                                                                                                                                                             SCHUBERT,
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                                                                                                      PROTEINS HAVING INSECTICIDAL ACTIVITIES
AND METHODS OF USE
11
                                                                                                                                                               KAREL
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8, 1997
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APPLICANT: Cigan, Amy L.
APPLICANT: Capla, Thomas H.
APPLICANT: Falls, Thomas H.
APPLICANT: Falls, Lynn
APPLICANT: Falls, Lynn
APPLICANT: Mayer, Terry E.
APPLICANT: Schubert, Scrt A.
APPLICANT: Schubert, Karel
TITLE OF INVENTION: Proteins Having Insecticidal Activities and Methods of TITLE OF INVENTION: Proteins Having Insecticidal Activities and Methods of TITLE OF INVENTION: Use
TITLE OF INVENTION: Use
CURRENT APPLICATION NUMBER: US/09/290,136
CURRENT APPLICATION NUMBER: 1999-04-13
EARLIER APPLICATION NUMBER: 1998-05-08
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 NETLLDQTTTNVVIPSF----DIKLLRPTIFSTFKLEEVPELNVKLSDVCMGTSAAPIVF 206
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Best Local Similarity 21.9%; Pred. No. 2.6;
Matches 51; Conservative 34; Mismatches
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21.9%; Pred. No. 2.6;
tive 34; Mismatches
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Patent No. 6339144
GENERAL INFORMATION:
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; ORGANISM: Pentaclethra macroloba
US-09-290-136-2
                                                           TELECOMMUNICATION INFORMATION TELEPHONE: 919 420 2202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51; Conservative
                                                                                                                                                            TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 408 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-09-074-912-4
                                                                                                                                                                                                                                                                                                                                                        amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Best Local S:
Matches 51
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APPLICANT: CIGAN, AMY L
APPLICANT: CIGAN, THOMAS H
APPLICANT: PALLS, LYNN
APPLICANT: PALLS, LYNN
APPLICANT: MUNDELL, SCOTT A
APPLICANT: SCHUBERY: SCOTT A
APPLICANT: SCHUBERY: KARE
TITLE OF INVENTION: PROTEINS HAVING INSECTICIDAL ACTIVITIES
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 408;
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STRET: 3605 GLENWOOD AVE.
CITY: RALBIGH
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE PORM:
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.1%; Score 77.5; DB Best Local Similarity 21.9%; Pred. No. 2.6; Matches 51; Conservative 34; Mismatches
APPLICATION NUMBER: US/09/074,912 FILING DATE:
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Patent No. 6057491
                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: SFROILL, W. WURRAY
REGISTRATION NUMBER: 32,943
REFERRENCE/DOCKET NUMBER: 5718
TELECOMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEPHONE: 919 881 3175
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ATTORNEY AGENT INFORMATION:
NAME: SPRUILL, W. MURGAY
REGISTRATION NUMBER: 32,943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-074-912-2
                                                                                                 CLASSIFICATION:
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APPLICANT: Cigan, Amy L.
APPLICANT: Cigan, Amy L.
APPLICANT: Pallis, Lynn
APPLICANT: Meyer, Terry E.
APPLICANT: Meyer, Terry E.
APPLICANT: Meyer, Terry E.
APPLICANT: Sabus, Brian
APPLICANT: Sabus, Brian
APPLICANT: Schubert, Karel
TITLE OF INVENTION: Use
FILE REFERENCE: 5718-9A, 035718/180486
CURRENT APPLICATION NUMBER: US/09/290,136
CURRENT APPLICATION NUMBER: US/09/290,136
CURRENT APPLICATION NUMBER: 09/074,912
EARLIER APPLICATION NUMBER: 09/074,912
SARLIER APPLICATION NUMBER: 09/074,912
SARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 4
LENGTH: 408
TYPE: PRT
ORGANISM: Pentaclethra macroloba
US-09-290-136-4
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Search completed: June 19, 2003, 15:05:27
Job time : 24 secs
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Patent No. 6339144
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                                                                                                              207 PPYYFKHGDTEFNLVDGAIIADIPA-----PVALSEVLQQEKYKN-KEIL 250
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                                                                                                                                                                                                                                                                              103 IEKL-----EIPTYICATDLYSGRALYLSEGSL--IPAL------LGSCAIPGIF 144
                                                                                                                                                                  145 EPVEYKN----YLLVDGGIVNNLPVEPFQESGIPTVCVDVLPIEPEKDIKNIL 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 LAIDGGGIRGIIPGVILKQLEATLQRWDSSARLAEYFDVVAGTSTGGIITAILTAPDPQN 98
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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Match
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(without alignments)
149.230 Million cell updates/sec
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           /cgn2_6/ptodata/1/pubpaa/PCT NEW FUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06 NEW FUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06 PEW PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US00_NEW PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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    9 US-10-027-805-39
9 US-10-027-804-39
9 US-10-027-804-39
9 US-10-147-026-10
10 US-09-765-205-40
9 US-10-034-337-10
9 US-10-034-337-10
9 US-10-034-337-10
10 US-09-815-242-5379
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US-10-027-804-36
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US-10-027-805-39
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/pubpaa/PCT_NEW_PUB.pep:*
/pubpaa/US06_NEW_PUB.pep:*
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 10, Appl
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US-09-903-410-36
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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RULL MURPHY, L TD, John An' PHY. Dennis

Anthony

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ALIGNMENTS	US-10-246-976-78	US-10-245-877-78	US-10-245-770-78	-473	-427-7	-185-7	-095-7	-880-	-621-		-409-	US-10-243-024-78	196-		-739-	US-10-245-730-78	-147-			Ψ			US-10-245-883-78	-10-245-851-	US-10-245-771-78	US-10-245-143-78
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FILE REPERENCE: DIVENTIBO-2
CURRENT APPLICATION NUMBER: US/09/903,410
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION UMBER: US 09/382,242
PRIOR APPLICATION UMBER: US 08/602,359
PRIOR FILING DATE: 1996-02-16
PRIOR FILING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.0
SEQ ID NO 36
LENGTH: 251 ; LENGTH: 251 ; TYPE: PRT ; ORGANISM: Aquifex pyrophilus US-09-903-410-36 Query Match 100.0%; Best Local Similarity 100.0%; Matches 251; Conservative (APPLICANT: PPLICANT: SWANSON, Ronald
PPLICANT: WARREN, Patrick
PPLICANT: WARREN, Patrick
PPLICANT: WARREN, Anna
TITLE OF INVENTION: ENZYMES HAVING ESTERASE ACTIVITY AND METHODS OF USE THEREOF 61 61 GMESLLKRVNWLKLFKFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICATDLYSG 1 LRLRKFEEINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPE RB11. MAFFIA, A... TNK, Steven Rona GMFSLLKRVNWLKLFKFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICATDLYSG LRLRKFEEINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPE 100.0%; Score 1273; DB 10; 100.0%; Pred. No. 1.2e-120; 0; Mismatches DB 10; 0; Indels Length 251; 0; Gaps 120 120 60 60

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us-09-903-410-36.rapb

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61 GMPSLLKRVNWLKLFKFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICATDLYSG 120
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                                                              181 LPIBPEKDIKNILHILLRSFFLAVRSNSEKRKBFCDLVIVPELEEFTPLDVRKADQIMER
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4225 EXECUTIVE SQUARE, STE 1400
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Pred. No. 7.6e-120;
0; Mismatches 1;
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRIT APPLICATION DATA:
APPLICATION NUMBER: US/10/027,804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: LINBAR
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION UNDRER:
APPLICATION UNDRER: 08/602,359
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ROBERTSON, Daniel E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                  MURPHY, Dennis
REID, John
MAFFIA, Anthony
LINK, Steven
SWANSOM, Ronald V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                    US-10-027-804-36
; Sequence 36, Application US/10027804
; Publication to US20030054530A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 251 AMINO ACIDS TYPE: AMINO ACID
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Best Local Similarity 99.6%;
Matches 250; Conservative
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STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
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                                                                               240
                                                                                                    RALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEPFQESGIPTVCVDV 180
                         121 RALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEPPOESGIPTVCVDV
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                                                                             LPIEPEKDIKNILHILLRSFFLAVRSNSEKRKEFCDLVIVPELEEFTPLDVRKADQIMER
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STREET: 4225 EXECUTIVE SQUARE, STE 1400
CITY: LA JOLLA
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1265; DB 9;
Pred. No. 7.6e-120;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/010001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 18M PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/027,805
FILING DATE: 21-Dec-2001
CLASSIFICATION: -(Unknown >
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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MOLECULE TYPE: PROPEIN

SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-027-805-36
                                                                                                                                                                                                                                                                                              Sequence 36, Application US/10027805
Fatent No. US20020164725A1
GENERAL INFORMATION:
MURPHY, Dennis
KEID, John
MAFFIA, Anthony
LINK, Steven
SWANSON, ROMAID
WARRIN, PAIRICK V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 251 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 619-678-5070 TELEPAX: 619-678-5099
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 99.6
Matches 250; Conservative
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    121
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RESULT 4
US-09-903-410-39
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/ ORGANISM: Aquifex VF5-34LC
US-09-903-410-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.0 SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39, Application US/09903410 Patent No. US20020146799A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 09/382,242
PRIOR FILING DATE: 1999-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MAFFÍA, Anthony
APPLICANT: LINK, Steven
APPLICANT: SWANSON, Ronald
APPLICANT: WARREN, Patrick
APPLICANT: WARREN, Patrick
APPLICANT: WARREN, Fatrick
APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ENZYMES HAVING ESTERASE ACTIVITY AND METHODS OF USE THEREOF
FILE REFERENCE: DIVER1180-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DIVERSA CORPORATION APPLICANT: ROBERTSON, Dan APPLICANT: MURPHY, Dennis
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PRIOR FILING DATE: 1996-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 71.8%; Score 913.5; DB 10; Length 249; Local Similarity 72.0%; Pred. No. 2.6e-84;
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                                                                                                                       LPITQERKIKNILHILIRSFFLAVRSNSEKRKEFCNVVIEPPLEEFSPLDVNKADEIF-C 243
                                                                                                                                             LPIEPEKDIKNILHILLESFFLAVRSNSEKRKEFCDLVIVPELEEFTPLDVRKADQIMER 240
                                                                                                                                                                                                    KALYFGRGDLIFVLLGSCSIFGIFEPVEYENFLLVDGGIVNNLFVEFLEKFKEFIIGVDV
                                                                                                                                                                                                                                                                                      EMLKLIKEVNWIKLFKFKTFKMGLMGWEKAAEFLEKELGVKRLEDINIFTYLCSADIYTG
                                                                                                                                                                                                                                                                                                                                                               GYIKALEVLSE
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                                          GDMRAL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROBERTSON, Dan
MURPHY, Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REID, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251
                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                         60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LENGTH: 249 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-027-805-39
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 70.8%; Score 901.5; DB 9; Best Local Similarity 71.5%; Pred. No. 4.3e-83; Matches 176; Conservative 31; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYRE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/027,805

FILING DATE: 21-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,359
PILING DATE: <Unknown>
ATTORNEY/ACENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/010001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 EXECUTIVE SQUARE, STE 1400
CITY: LA JOLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                               185
                                     241 GYIKAL 246
                                                                                                                       181
                                                                                                                                                                                 121 RALYLSEGSLIPALLGSCAIPGIPEPVEYKNYLLVDGGIVNNLPVBFPQESGIPTVCVDV 180
                                                                                                                                                               125 KALYFGRGDLIÞVILGSKSIÞGIFEÞVEYENFLLVDGGIVNNLÞVEFLEKFKEÞIIGVDV 184
                                                                                                                                                                                                                                            65 EMLKLIKEVNWIKLFKFKTPKWGLMGWEKAAEFLEKELGVKRLEDLHIFTYLCSADLYTG 124
                                                                                                                                                                                                                                                                                    61 GMFSLLKRVNWLKLFKFKPPLKGLIGWEKAIRFLBEVLPYRRIEKLHIPTYICATDLYSG 120
                                                                                                                                                                                                                                                                                                                              u
                                                                                                                                                                                                                                                                                                                                                  1 LRLRKFEEINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPE 60
GDMRAL 249
                                                                                                            LPIEPEKDIKNILHILLRSFFLAVRSNSEKRKEFCDLVIVPELEEFTPLDVRKADQIMER 240
                                                                                                                                                                                                                                                                                                          LKLKRFÉEVNLVLSGGAAKGIAHIGVLKALEELGIKVKRLSGVSAGNIVSVFYASGYTPD
                                                                               LPITQERKIKNILHILIRSFFLAVRSNSEKRKEFCNVVIEPPLEEFSPLDVNKADEIF-C 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10027805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WARREN, Patrick V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROBERTSON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAFFIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MURPHY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anthony
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Gaps

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RESULT 5

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62 MPSLLKRVNWLKLFKFKPPLKGLIGWEKAIR-FLEEVLPYRRIEKLEIPTYICATDLYSG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 RALYLSE----GSLIPALLGSCAIP---GIFEPVEYKNYLLVDGGIVNNLP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.0%; Score 139.5; DB 9; Length 425; 23.2%; Pred. No. 1e-05; Live 41; Mismatches 104; Indels 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 VSPY--GEHDICPKVKSTNFLQVNITNLSLRLCTGNLHLLTRALF
                                                                                                                                                                                                                                                          Pain Genes; Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 DLVIVPELEBFTPLDVRKADQIMERGYIKALEVLSE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WS-10-147-026-10

Sequence 10, Application US/10147026

Publication No. US2003003538A1

Publication No. US2003003538A1

APPLICANT: Dietrich, Paul Shartzer

APPLICANT: Buang, Chiao-Chain

APPLICANT: Sangameswaran, Lakshim

TITLE OF INVENTION: Neuropathic Pain Genes; Compos;

TITLE OF INVENTION: Neuropathic Pain Genes; Compos;

TITLE OF INVENTION: Neuropathic Pain Genes; Compos;

TITLE OF INVENTION: Neuropathic Pain Genes; COMPOS;

CURRENT APPLICANTON: NOUNBER: US/10/147,026

CURRENT APPLICATION NUMBER: 60/155,702

PRIOR APPLICATION NUMBER: 60/155,702

PRIOR APPLICATION NUMBER: 60/189,931

PRIOR APPLICATION NUMBER: 60/189,931

PRIOR APPLICATION NUMBER: 60/189,931

PRIOR PELING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PaatSEQ for Windows Version 4.0

LENGTH A. 255
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244 GDMRAL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: rattus sp.
US-10-147-026-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 RALYLSEGSLIPALLGSCAIPGIFEPVEYRWYLLVDGGIVNNLPVEPFQESGIPTVCVDV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 LPIBPBKDIKNILHILLRSFFLAVRSNSEKRKEFCDLVIVPELBEFTPLDVRKADQIMER 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
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                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: FISH & RICHARDSON P.C.
STREET: 4225 EXECUTIVE SQUARE, STE 1400
CITY: ita JOLLA
STATE: CALIFORNIA
COMPUTER: LALIFORNIA
COMPUTER: RENDABLE PORM:
MEDLIOM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: MORD PERFECT 6.0
CURRENT APPLICATION UDBERS: US/10/027,804
FILING DATE: 21-Dec-2001
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,359
FILING DATE: «Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/010001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
TOPOLOGY: LINEAR

NOLECTLE TYPE: PROFEIN

SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-027-804-39
                                                                                                                                                                                     MAPFIA, Anthony
LINK, Steven
LINK, Steven
SWANSON, Ronald V.
WARREN, Patrick V.
KOSNOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
                                                             Sequence 19, Application US/10027804
Publication No. US/2030054530A1
GENERAL INFORMATION:
APPLICANT: ROBERTSON, Daniel E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 619-678-5070
TELEPRAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 249 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                   MURPHY, Dennis
REID, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GYIKAL 246
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US-10-034-937-14
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SEQ ID NO 14
LENGTH: 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/10034937
Publication No. US20030097684A1
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                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/260,477
PRIOR FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Lipid Acyl Hydrolases and Variants Thereof
FILE REFERENCE: 18097A-032010US
CURRENT APPLICATION NUMBER: US/10/034,937
CURRENT FILING DATE: 2002-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Carr, Brian
APPLICANT: Rosen, Barl
APPLICANT: Bermudez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence:clone PIP-10 OTHER INFORMATION: improved pentin lipid acyl hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
mes 69; Conserv
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                           189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 L----SEGSLIPALLGSCAIP---GIFEP----VEYKNYLLVDGGIVNNLP------ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 FIEVSKEARKRPLGPLHPSFNLVKLIRSFLLKVLPADSHEHASGRLGISLTRVSDGENVI 128
                                                                                                                                                                                                                                                                                                                                                                       11 LVLSGGAAKGIAHIGVLKAIN------ELGIRVRALSGVSAGAIVSV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 NLVLSGGAAKGIAHIGVLKAINE----LGIRVRALSGVSAGAIVSVFYASGYSPEGMFSL 65
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                                                                      EPVEYKN----YLLVDGGIVNNLPVEPFQESGIPTVCVDVLPIEPEKDIKNIL 193
                                                                                                                       NETLLDQTTTNVVIPSF----DIKLLRPTIFSTFKLEEVPELNVKLSDVCMGTSAAPIVF
                                                                                                                                                                         IEKL------EIPTYICATDLYSGRALYLSEGSL--IPAL-----LGSCAIPGIF 144
                                                                                                                                                                                                                       KDRPLYAAGEIIDFYIEHGPSIFNKSTACSSPGIFCPKYDG-----KYLQEIISQKL 132
                                                                                                                                                                                                                                                                                                                         LAIDGGGIRGIIPGVILKQLEATLQRWDSSARLAEYFDVVAGTSTGGIITAILTAPDPQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---PLVLR---EMCKQGYRDGLRFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSPF--SGESDIC-----PODSSTNIHE--LRVTNTSIQFNLRNLYRLSKALFPPE-- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEPFQESGIPTVCVDVLPIBPEKDIKNILHILLRSFFLAVRSNSEKRKEFCDLVIVPELE 224
                                                                                                                                                                                                                                                                        ----FYASG-----YSPEGMFSLLKRVNWLKLFKFKPPLKGLIGWEKAIRFLEEVLPYRR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ness, Jon E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.6%; Score 109.5; DB 10; Length 504; 26.0%; Pred. No. 0.014; ative 32; Mismatches 115; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86.5; DB 9; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249
                                                                                                                                                                                                                                                                                                                                                                                                                           79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                           71;
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US-10-160-758-11
                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/160,758
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-10
PRIOR PILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
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; ORGANISM: Homo sapiens
US-10-160-758-12
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SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 3354
                                                                                                  SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: CADS AS MODIFIERS OF THE
FILE REFERENCE: EX02-089C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.7%; Score 85.5;
Best Local Similarity 21.3%; Pred. No. 54;
Matches 53; Conservative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/10160758
Publication No. US20030036076A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/10160758 Publication No. US20030036076A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/160,758
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
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TITLE OF INVENTION: CADS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EX02-089C
                                              LENGTH: 33
TYPE: PRT
                                                                                                                                             NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 NYLL----VDGGIVNNLPVEPFQESGIPTVCVDVLPIE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 LKRVNW------CKLFKFKPPLKGLI------GWEKAIRFLEEVLP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 AHIGVLK----AINELGIRVRA-------LSGVSAGAIVSVFYASGYSPEGMFSL 65
                                                                      3354
                                                                                                                       PatentIn
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                                                                                                                          version
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----PE 186

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APPLICANT: Thym, Detlef
APPLICANT: Thym, Detlef
APPLICANT: Knappe, Wolfgang-Reinhold
APPLICANT: Shao, Zhixin
APPLICANT: Schmuck, Rainer
APPLICANT: Schmuck, Rainer
APPLICANT: Bunk, Daniella
TITLE OF INVENTION: Debydrogenase
TITLE OF INVENTION: Debydrogenase
TITLE OF INVENTION: 2001-12-19-29
FILE REFERENCE: ROID 00112CIPUS
CURRENT APPLICATION NUMBER: US/10/082,627A
CURRENT PILING DATE: 2000-10-27
FRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344 YICWPTVAPSSA-YVYTG-----GKKAIPG-----WENTLLVPSLKRGVIFRIKLDP 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 YICATDLYSGRALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLVDG---GIVNNLPVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 EEINLVLSGG------AAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168, FOESGIPTVCVDVLPIEPEKDIKNILHILLRSFFLAVRSNSEKRKEFCDLVIVPE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 TYS----TYLDDAIPM-------FKSNNRYR----DVIASPE 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67; Indels 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Object, Kari L.
APPLICANT: Colsen, Kari L.
APPLICANT: Rall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramotoc, Robert T.
APPLICANT: Vamamotoc, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: 12 Prokaryotes
FILE REFRENCS: ELITRA, 0.11A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
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22.1%; Pred. No. 5.2;
tive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5379, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 22.18 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-815-242-5379
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 NKGRPLYAAEBIINFYIEHGPSIFNKSTACSLPGIFCPKYDG------KYLQEIISQK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----RIEKLEIPTYICATOLYSGRALYLSEGSL--IPAL-----LGSCAIPGIFEPV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 INETRIDC/TTTNVVIPSFDIKLIRPTIFSTFKLÆEVPELNVKLSDVCMGTSAAPIVFPPY 191
                                                                                                                                     100 YRRIEKLEIPTYICATULYSGR ----ALYLSEGSL --- IPALLGSCAIPGIFEPVEYK 150
                                                                                                                                                                                                                                                                                                                                                      582 -ENIMAGATVLFINATDLDRSREYGQESIIYSLEGSTQFRINARSGEITTTSLLDRETKS 740
                                                                                                                                                                                                                                                                                                                                                                                                                151 NYLL----VDGGIVMNLPVEPFQESGIPTVCVDVLPIE-------PE 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 6.6%; Score 83.5; DB 9; Length 390;
Best Local Similarity 20.9%; Pred. No. 4.1;
Matches 48; Conservative 40; Mismatches 77; Indelø 65; Gaps
                                                                                                      ----LSGVSAGAIVSVFYASGYSPEGMPSL
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence:clone PIP-6; OTHER INFORMATION: improved pentin lipid acyl hydrolase US-10-034-937-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 YPKHGDTEFNLVDGAIIADIPA------PVALSEVLQQEKYKN-KEIL 232
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Ouery Match 6.7%; Score 85.5; DB 9; Length 3354; Best Local Similarity 21.3%; Pred. No. 54; Matches 53; Conservative 36; Mismatches 75; Indels 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen, Barbara A.
APPLICANT: Resen, Barbara A.
APPLICANT: Resen, On E.
APPLICANT: Ness, Jon E.
APPLICANT: Maxyelson, Inc.
TITLE OF INVENTION: Lipid Acyl Hydrolases and Variants Thereof
FILE REFERENCE: 18097A-032010US
CURRENT APPLICATION NUMBER: US/10/034,937
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 60/260,477
PRIOR APPLICATION NUMBER: US 60/260,477
PRIOR PILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/10034937
Publication No. US20030097684A1
GENERAL INFORMATION:
                                                                                                      22 AHIGVLK --- AINELGIRVRA
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795 SDVT-TVVAV 803
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LENGTH: 390
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APPLICANT: KU, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes

PILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PILLING DATE: 2000-03-21

PRIOR PILLING DATE: 2000-05-26

PRIOR PILLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/242,578
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US-09-815-242-12285
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR TILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PELICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR PILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
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SOFTWARE: FRANCED for Windows Version 4.0
SEQ ID NO 5379
LENGTH: 391
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                        APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASE-SEQ for Windows Version 4.0
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Search completed: June 19, 2003, 15:13:00 Job time : 183 secs

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Result
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    SwissProt_40:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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	97). GS T	wa H.F., Z e sequence	¥. ~	, Schle ska A., B., Ta	P., Pur P., Pur C., Roc	R.P., M	er P., A., Lar	J., Hag	ton J., Fujit	L'L', B	PubMed=9384377 a N., Moszer I	n E., Glaser chromosomal) to the EMB	s; Baci	9, Created) 9, Last seq 1, Last anno n ylbK.	DARD;		1884 292 1435 1564 1698 1246 1246 1729 1729 1729 1729 1759
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	028 (SWS) FAMILY.	0 0 0	Terpstra P., Vannier F., er H., Weitze	, Schroeter R., Scoffone F., S.J., Serror P., Shin B.S., ., Takahashi H., Takemaru K.	B., Rapoport G., Rey M., Reyno' Roche B., Rose M., Sadaie Y.,	Moestl D., Nakai S., Nak iwara A., Oudega B., Park	in G., Krogh S., Ku , Lauber J., Lazare	ech J., Harwood C.F., Hullo M.F., Itaya	A., Enriich S.D., ., Ferrari E., Foul a S., Galizzi A., C	raun M., B B., Capua F., Cummin	Albertini A.M., All	<pre>Ser P., Richou A., Danchin ual region downstream nprB." EMBL/GenBank/DDBJ databases</pre>	Bacillaceae; Bacillus	e update) ion update)	260 AA.	ALIGNMENTS	0 5 2 2 0 5 E
	hrough a	0 E 25	Tognoni A. Vassarotti enegger T.,	n B.S.,	scott A.m., M., Reynolds adaie Y.,	S., Noback	Kumano M., arevic V.,	R., Henaut	E., Foulger D., zi A., Galleron N.	S.C., B Sarter N Daniel	Alloni G.,	86	18.				Q14690 P28845 P28845 P4031 O74020 Q38424 Q9zkc0 Q9zk0
	collaboration	ta K., n A.; Bacillus	Α.,	Soldo B.,	M., olds S.,	ck M., S.H.,	, 5	nes Det	N.,	R. M.							homo sapien homo sapien bradyrhizob pyrococcus bacteriopha helicobacte mus musculu synechococc bacillus me thermotoga mus musculu schizosacch

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MEDLIRE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Rlay M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94110230; PubMed=8282700; Sepel M., Kersten H.; Resid M., Kersten H.; Rorganization and functions of genes in the upstream region of tyry of Escherichia coll: phenotypes of mutants with partial deletion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypochetical protein ychK.

YCHK OR B1234.
Bschericha coli.
Bacteria, Proteobacteria; gamma subdivision; Enterobacteriaceae;
Bscherichia.

NCBI_TaxID=562;
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                                                                                                                                                                                 21.1%; Score 268.5; DB 1; Length 260; 28.2%; Pred. No. 4.7e-17; ive 54; Mismatches 106; Indels 13;
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"The complete genome sequence of Escherichia coli K-12.";
                                                                                                                            Pfam, PF01734, Patatin, 1.
PROSITE, PS0127, UPF00128, 1.
Hypothetical protein; Complete proteome.
SEQUENCE 260 AA; 28258 MW; 363B6DDF017BE77B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriol. 176:221-231(1994).
                                                                                            Subtilist; EG13363; ylbK.
InterPro; IPR002641; Patatin.
InterPro; IPR001423; UPF0028.
                                                                         EMBL; 298682; CAB11357.1; -.
                                                                                                                                                                                          Similarity 28.2 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                     Z99111; CAB13377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=K12;
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                                                                                                                                                                                                                                                                                                                                                                                                      241
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 ATDLYSGRALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLFVEPPQESGI 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=8905232;
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masdida S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Namura Y., Vashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12,7-28.0 min region on the linkage map.";
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Live 48; Mismatches 107; Indels
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PROSITE; PS01237; UPF0028; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 314 AA; 34355 MW; 5ABBDE877C72FE40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA RES. 3:137-155(1996).
-!- SIMILARITY: BELONGS TO THE UPF0028 (SWS) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 PTVCVDVLPIEPEKDIKNILHIL---LRSF------
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EMBL; AE000221; AAC74316.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interPro; IPR002641; Patatin.
interPro; IPR001423; UPF0028.
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EcoGene, EG12120; ychK.
Science 277:1453-1474 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 3:363-377(1996)
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Query Match
Best Local S
Matches 79
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STRAIN-5288c / AB972;
DEVLIN K., Churcher C., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ database;
Submitted (NOV-1994) TO THE UPF0028 (SWS) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entitles requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002641; Patatin.
InterPro; IPR00123; UPP0028.
InterPro; IPR000595; cNMP_binding.
Pfam; P60027; cNMP_binding; 2.
Pfam; P60734; Patatin; 1.
SMART; SM00100; cNMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z46729; CAA86716.1; -. SGD; S0004524; YML059C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Ref. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
14-CCT-2001 (Rel. 40, Last annotation update)
15-CCT-2001 (Rel. 40, Last annotation update)
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01-NOV-1997
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TRANSMEM
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                                                                                                                                                                                                                                                                                         1 LRLRKF---EEINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGY
                                                                                                                                                                                                                                                                                                                                                            Similarity
 SNSEKRKEFCDLVIV-PELEEFTPLDVRKADQIMERG
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                                                                                                                                                                                               DLVPIYGRVKKFAGRISSIWRMLTDLTWPVTSYTTGHEFNRGIWKTFGDTRIEDFWIQYY
                                                                                                                                                                                                                                                                    LRLARILSGQAIGLVLGGGGARGISHLGVIQAIEEQGIPVDVIGGTSIGSFVGGLYAKDY
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PS01237; UPF0028; 1.
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                                                     GCQTIFAVDVGSADDRTPMEYGDSLNGFWIIFNRWNPFSSHPNIPNMAEIQVRLGYVASV
                                                                                          GIPTV-CVDV-----
                                                                                                                            CNSTNITDSVQEIHSFGYAWRYIRASMSLAGLLPPLEENGSMLLDGGYVDNLPVTEMRAR
                                                                                                                                                           ICATDLYSGRALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEPFQES
                                                                                                                                                                                                                                SPEGMESLLK----RVN--WIKLEKEKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTY
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1679 AA;
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                         42; Mismatches
                                                                                                                                                                                                                                                                                                                                                        Score 242;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                        DB 1;
.2e-13;
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                                                                                          -LPIEPEKDIKNILHILLRSFFLAVR 205
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YCHK SHIFL
     SAE
                                                     RESULT 5
YP65_MYCTU
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Best Local S
Matches 58
YP65 MYCTU
Q50733;
01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rudd K.E.;

Unpublished observations (FEB-1994).

-i- SIMILARITY: BELONGS TO THE UPFO028 (SWS) FAMILY.

-i- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAME
BE INTRODUCED IN POSITION 178 TO PRODUCE THIS ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-entropean.or.ent.)
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01-JUN-1994 (Rel. 29,
16-OCT-2001 (Rel. 40,
Hypothetical 34:4 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hromockyj A.E., Tucker S.C., Maurelli A.T.;
"Temperature regulation of Shigella virulence:
repressor gene virR, an analogue of hms, and pa
by tyrosyl transfer RNA (tRNA1(Tyr)).";
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X66849; -; NOT ANNOTATED CDS. InterPro; IPR002641; Patatin. InterPro; IPR001423; UPF0028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01734; Patatin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONCEPTUAL TRANSLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Microbiol. 6:2113-2124(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93023838; PubMed=1406252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Serotype 2A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shigella.
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                                                                                                                                                             114
                                                                                                                                                                                                                                63
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                                                                                                                                                                                                                                                                    14
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                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                         LRKFEEINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS01237; UPF0028; 1.
                                                                                                                                                                                               LSALE--DWVTSFSYWELLRLMDLSWQRGGLLRGERVFNQYREIMPETEIENCSRRFAPV 125
                                                                                                                                                                                                                                FSLLKRVNWLKLEKEKPPLK------GLIGWEKAIRFLEEVLPYRRIEKLEIPTYIC 113
                                                                                                                                                           ATDLYSGRALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPV 165
                                                                                                                                                                                                                                                                    MRKI-KIALALGSGAARGWSHIGVINALKKVCIEIDIVAGCSIGSLVGAAYAC----
                                                                                                                            ATNLSTGRELWFTEGDLHLAIRASCSIPGLMAPVAHNGYWLVDGAVVNPIPI 177
                                                                                                                                                                                                                                                                                                                                                                                                            192 AA;
 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                      STANDARD;

    Last sequence update)
    Last annotation update)
    kDa protein in HNR-PURU intergenic

                                                                                                                                                                                                                                                                                                                                                                                                        192
20831 MW;
                                                                                                                                                                                                                                                                                                                                                      18.7%;
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                                                                                                                                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                      Score 237.5; DB 1
Pred. No. 2.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                            34AEF6A693CC917A CRC64;
                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192
                                      583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                    B
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                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                         64;
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                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                        Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restrictions on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL
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collaboration outstation

SOUTH TERM TO THE

8 B \$ 밁 8

17;

Gaps

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В Ś 밁

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its modified and this statement is not removed. Usage by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
172 GIPTVCVD------VLP--IEPEKDIKNIL-------HILLRSFFLAVRS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Pleischmann R.D., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolomay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=H37RV;
MEDLINE=99295897; PubMed=9634230;
Gordon S.T., Barosch R., Parkhill J., Garnier T., Churcher C.; Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Reltwell T., Gentles S., Hamlin N., Holroyd S., Harnsby T., Jagels K., Krojh A., McLen J., Moule S., Murphy L., Oliver S., Osborne J., Rush A., McLen J., Moule S., Murphy L., Stelton S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
Bacteria, Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
WCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bishai W.; "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE UPF0028 (SWS) FAMILY.
                                                                                                                                                                                                                                                                                             1 protein; Complete proteome.
360 AA; 37522 MW; F0BC30CE6096D0F6 CRC64;
                                                                                                                                                                                                                                                   207 NSEKRKEFCDLVIVPELEEFTPLDVRKADQIMERGYIKALEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein Rv1063c.
RV1063C OR MT1093 OR MTV017.16C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01734; Patatin; 1.
PROSITE; PS01237; UPF0028; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL021897; CAA17179.1; -. EMBL; AE006990; AAK45347.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuberculist, Rv1063c; -.
InterPro; IPR002641; Patatin.
InterPro; IPR001423; UPF0028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 393:537-544 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | | : : | | | : | | | | : : | | | : : | | | : | | | : | | | | : | | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 CATDLYSGRALYLSEGSLIPALLGSCAIPGIFEPVEYRNYLLVDGGIVNNLPVEPF-QES 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann S.D., Alland B., Gwinn M.L., Haft D., Hickey E.,
Kolomay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 INLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56; Gaps
                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98295987; PubMed=9634230;

Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia P. Badcock K., Basham D., Chillingworth T., Connor R., Badcock K., Basham D., Erown D., Chillingworth T., Connor R., Davies R., Daviln K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares S., Squares R., Sulfer S., Stafates S., Squares R., Sulfec J., Taylor K., Whitehead S., Barrell B.G., Barrell B.G., Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.5%; Score 235; DB 1; Length 583; 24.7%; Pred. No. 1.4e-13; ive 51; Mismatches 106; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE UPF0028 (SWS) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 375 G -> D (IN REF. 2).
583 AA; 62123 MW; ECGEBO62BAEC62F7 CRC64;
                                              annotation update)
01-NOV-1997 (Rel. 35, Last sequence update)
L-JUN-2002 (Rel. 41, Last annotation update)
Hypotherical protein RV2565.
RV2565 OR MT2641 OR MTCY964.03C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PS5042; CWNP EINDING 3; 1.
PROSITE: PS01237; UPP0028; 1.
PROPHELICAL protein; Complete proteome.
CONFLICT 375 375 G -> D (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuberculist, Rv2565; -.
InterPro; 1PR002641; Paratin.
InterPro; 1PR001423; UPP0028.
InterPro; 1PR000595; cNMP_binding.
Pfam; PR001007; cNMP_binding; 1.
Pfam; PR01734; Paratin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z77250; CAB01050.1; -. EMBL; AE007098; AAK46954.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete genome sequence.";
Nature 393:537-544 (1998).
                                                                                                                                           Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 24.78

1es 70; Conservative
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       NCBI TaxID=1773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bishai W.;
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Best Loc Matches

Loca1

Similarity

33.1%;

Pred. No.

Mismatches

9.4e-14; ches 67;

Indels

18;

Gaps

Conservative

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                                                                              RX KURDLINE-98044033; PubMod=9384377;
RX KUNST F. Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borviss R., Boureier L., Brans A., Braum M., Brignell S.C., Bron S.,
RA Borviss R., Boureier L., Brans A., Eraum M., Brignell S.C., Devone K.C., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Galizzi A., Galleron N.,
RA Chis S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Haga K., Haeer-Blanchard M., Klain C.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Hapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parrov V., Pohl T.M., Portteclle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Schleib S., Schleib S., Schleib S., Schleib S., Schroeter R., Scoffone F.,
RA Sekiguchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viani A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Vasamoto K., Vata K.,
Voshikawa H., Danchin A.,
Voshikawa H., Danchin A.,
Voshikawa H., Danchin A.,
Voshikawa H., Danchin A.,
Ra Voshida K., Yoshikawa H., Danchin A.,
Ra Voshida K., Yoshikawa H., Scoffone
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Kobayashi Y.;
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Mizuno M., Masuda S., Takemaru K.-I.,
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Bacteria; Firmicutes;
NCBI_TaxID=1423;
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(Rel. 34, Last sequence update)
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Matches 80
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EMBL; Z99116; CAB14382.1; --
Subtilist; BG11703; yqho.
InterPro; IPR002641; Patatin.
Pfam; PF01734; Patatin; 1.
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242
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                          KEFCDLVIVPELEE---FTPLD
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RESULT
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       SULT 8
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QSUG69; QSW3M0;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequents-JUN-2002 (Rel. 41, Last annot

Swiss cheese protein.

SWS OR CC2212
   MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., E.
Amanatides P.G., Scherer S.E., Li P.W.,
George R.A., Lewis S.E., Richards S., Av
                                                                                                   MEDLINE=97442511; PubMed=9295388; Kretzschmar D., Hasan G., Sharma S., I "The swiss cheese mutant causes glial degeneration in Drosophila."; J. Neurosci. 17:7425-7432(1997).
                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacca; Hexapoda;

Insecta; Peteryota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                         SEQUENCE FROM
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PMENTAL STAGE,
                                                                                                                                                                                                                                                                                                                           sequence update) annotation updat
                                                                                                                                                                                   ALTERNATIVE SPLICING, 'AGE, AND MUTAGENESIS OF
                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                  1425
                                                                                                                            Heisenberg M.,
l hyperwrapping
Evans C.A., Gocayne J.D.
', Hoskins R.A., Galle R.
Ashburner M., Henderson
                                                                                                                                                                                                                                                                                                                           update)
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                                                                                                                                                                                   TISSUE
F GLY-648
                                                                                                                               and brain
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Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brill J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Bauster B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Bauster B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Baus A., Baxendale J., Bayraktaroglu L., Besaley E.M.,
RA Burkis K.C., Busam D.A., Butler H., Gadieu E., Center A., Chandra I.,
RA Burkis K.C., Busam D.A., Butler H., Gadieu E., Center A., Chandra I.,
RA Cavley S., Dahlek C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Plakove B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischman W.,
RA Burkis N.L., Harvey D., Haiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Havyer D., Haiman T.J., Hernandez J.R., Houck J.,
Allali M., Kalueh F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
Jalai M., Kalueh F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Ilu X., Mattei B., McThtosh T.C., McLeod M.P., Morberson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Noute S.M., Nelson K.A., Wixon K., Purky D.M., Pacleb J.M.,
Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rese M.G.,
Reinert K., Remington K.A., Shangon M., Strong R., Shen H.,
Spier R., Speaching A.C., Stapleton M., Strong R., Shen H.,
Syiekas R., Tector C., Turner R., Vohler S., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Radibas R.A., Whore S.W., Rubing G., Zhan Q., Zhan Q., Zhan Q., Zhan Q., Zhan Q., Zhan Q., Zhan Q., Zhan Q., Zhan Q., Zhan Q., Zhan Q., Zhan Q., Zhan Q., Zhan Q., Zhan Q., Zhan Q., Zhan Q., Zhan Q., Zhan Q., The Geneme Sequence of Drosophila melanogaster.;
The genome sequence of Drosophila melanogaster.;
FINCTION. NEURON AND STATEMENT OF THE SIGNALING MECHANISM BETWEEN METRONS AND GLIA THAT REGULATES GLIA WRAPPING DURING DEVELOPMENT OF THE ADULT BRAIN.

-I ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT PORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

-I SHORT PORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

-I SEVELOPMENTAL STAGES WITH HIGHEST LEVELS IN YOUNG EMBRYOS AND DEVELOPMENTAL STAGES WITH HIGHEST LEVELS IN YOUNG EMBRYOS AND ADULTS. THE SHORT ISOFORM IS DETECTED ONLY IN ADULT

SIMILARITY: BELONGS TO THE UPP0028 (SWS) FAMILY. CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.

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PROSITE; PS50042; CNMP BINDING 3; 3. EMBL; 297187; CAB51772.1; -. EMBL; AE003442; AAF46305.1; ALT_SEQ. FlyBase; FBgn0003656; sws. InterPro; IPR002641; Patatin.
InterPro; IPR001423; UPF0028.
InterPro; IPR000595; CMP binding.
Pfam; PF00027; CMP binding; 3.
Pfam; PF01734; Patatin; 1.
SMART; SM00100; CMMP; 2.

Alternative splicing; Developmental protein.

Alternative splicing; Developmental protein.

MUTAGEN 648 648 G-SR: IN ALLELE SWS-5; AGE-DEPENDENT NEURODEGENERATION.

MUTAGEN 956 956 G->D: IN ALLELE SWS-4; AGE-DEPENDENT PROSITE:

: : | | | : | | : | | : | 1.25 1126 IAIDVGSQDDTDLTNYGDDLSGWWLLYKKWNPFTSPVKVPDLPDIQSRL----AYVSCV 1180 67 -----KRVNW-LKLFKFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICATDLY 118 119 SGRALYLSEGSLIPALLGSCAIPGIFEPV--EYKNYLLVDGGIVNNLPVEPFQESGIP-T 175 9 INLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGMFSLL--176 VCVDV------LPIEPEKDIKNILHILLRSFFLAV Gaps 55, Length 1425; Indele NEURODEGENERATION. 1425 AA; 160594 MW; 2A7AF2DAC06FE553 CRC64; 205 RSNSB-KRKEFCDLVIVPELEEFTPLDVRKADQIMERGYI 243 ; Pred. No. 1.6e-11; 44; Mismatches 108; DB 1; 17.1%; Score 217.5; 26.1%; Pred. No. 1.6 Query Match
Best Local Similarity 26...
Best T3; Conservative SEQUENCE 5 F 셤 엄 ò ò ò g ò 셤

Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis. YOL4 CAEEL STANDARD; PRT; 1371 AA. 002331, QSSEN1; 205211, 2002311, 2002511 SEQUENCE FROM N.A. STRAIN-Bristol N2; MEDLINE=94150718; PubMed=7906398; Caenorhabditis elegans. NCBI_TaxID=6239;

CAEEL RESULT 9

Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraer A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Liloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Riken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer B., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; a and b (shown here); may be produced by alternative splicing.
-!- SIMILARITY: BELONGS TO THE UPF0028 (SWS) FAMILY.

REVISIONS, AND ALTERNATIVE SPLICING.

Waterston R.;

Nature 368:32-38(1994).

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Best Local
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PROSITE; PS01237; UPF0028; 1.

PROSITE; PS01237; UPF0028; 1.

Hypothetical protein; Alternative splicing.

Hypothetical protein; Alternative splicing.

Hypothetical protein; Alternative splicing.

Hypothetical protein; Alternative splicing.

Hypothetical protein; Alternative splicing.

Hypothetical protein; Alternative splicing.

Hypothetical protein; Alternative splicing.

Hypothetical protein; Alternative splicing.

Hypothetical protein; Alternative splicing.
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein Millo.7 in chromosome II.
Millo.7.
                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the Buropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    InterPro; IPR002641; Patatin.
InterPro; IPR001423; UPF0028.
InterPro; IPR000595; cNMP binding.
Pfam; PF00027; cNMP binding; 3.
Pfam; PF01734; Patatin; 1.
SMART; SM00100; cNMP; 2.
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                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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WormPep; ZK370.4b; CE29641.
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Z49966; CAA90246.1;
Z49968; CAA90246.1;
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      JOINED
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RESULT 11
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Best Local
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InterPro; IPR000595; cNMp binding.
Pfam; PF00027; cNMp binding; 1.
Pfam; PF01734; Patatin; 1.
SMART; SM00100; cNMP; 2.
                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 102.7 kDa protein in PRP16-SRP40
YKR089C OR YKR409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 880 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z49968; CAA90264.1;
EMBL; Z49966; CAA90264.1;
WormPep; M110.7; CE03510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50042; CNMP_BINDING_3; PROSITE; PS01237; UPF0028; 1.
                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
MEDLINE=94262327; PubMed=8203164;
                                                                                                                                                                                    P36165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002641; Patatin.
                SEQUENCE FROM N.A.
                                          NCBI_TaxID=4932;
                                                                                                                                                                                                   YEAST
                                                                                                                                                                                                                                                                                                                                      721
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                                                                                                                                                                                                                                                                             781 CCVNOMEIVKNAOYCYYVKLP-IESFGIFDFSKFDQAAQIGY
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                                                                                                                                                                                                                                                                                                                                                                                                  CITTDLTSSSMRIHRNGIMMPVVRSSMSIAGYVPPICDPQDGHLLLDGAYVNNLPADIMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFFTDRERNNIEDVVRDETW-----PYCGILTGHRENECVQRWENDVNIEDCWVSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPE-----
                                                                                                                                                                                                                                                                                                       AVRSNSE--KRKEFCDLVIVPELEEFTPLDVRKADQIMERGY
                                                                                                                                                                                                                                                                                                                                     SLGANVVIAIDVGMSDDNTNLRNYGFSISGTWCLFKRWWPFGEELRVLNMNEVQNRLAYV
                                                                                                                                                                                                                                                                                                                                                                    ESGIPTY-CVDV-----
                                                                                                                                                                                                                                                                                                                                                                                                                          ICATDLYSGRALYLSEGSLIPALLGSCAIPGIFEPV--EYKNYLLVDGGIVNNLPVEPFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GMFSLLKRVNWLKLFKFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTY 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGIVFGGGGARGAAHAGALRALIEKKVQIDMVGGTSIGALFGSLYAT--TPDIRAVGRMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100053 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45;
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Pred. No. 3e-
                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                      intergenic region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                             821
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                                                                                                                                                                                                                                                                                                                                        780
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                                                                                                                                                                                                      Garcia-Cantalejo J., Baladron V., Esteban P.F., Santos M.A., Bou G Remacha M.A., Revuelta J.L., Ballesta J.P.G., Jimenez A., del Rey "The complete sequence of an 18,002 bp segment of Saccharomyces cerevisiae chromosome XI contains the HBS1, MRP-L20 and PRP16 gene and six new open reading frames.";
                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                     -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: TO YEAST YMR313C AND S.POMBE SPCC1450.16C.
                                                                                                                        the Swiss Institute
                                                                                                                      of Bioinformatics
                                                                                                                        and the
                                                                                                                                                                                                                                            and PRP16 genes,
                                                                                                                        EMBL outstation
                                                                                                                                       a collaboration
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EMBL; Z27116; CAA81640.1;

11;

52; Gaps

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                                                                                                                                                                                                                                                                                                          69 TILKVVSQARSRIFGPLHPBFNLLGIVRDE----LEVILP-----PN---AYEMC 111
                                                                                 7 EEINLVLSGGAAKGIAHIGVLKAINELG--IRVRALSGVSAGAIVSVFYASGYS-PEGMF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee W.-C., Salido E., Yen P.H.;
"Isolation of a new gene GS2 (DXS1283E) from a CpG island between STS and KALl on Xp22.3.";
Genomics 22:372-376(1994).
-!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED, INCLUDING HEART, BRAIN, PLACENTA, LUNG, LIVER, MUSCLE, KIDNEY, PANCREAS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 BEINLVLSGGAAKGIAHIGVLKAINELGIR----VRALSGVSAGAIVSVFYASGYSPEGM
                                                                                                                                                                              64 SLLKRVNWLKLFKFKP-----PLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICATDLY
                                                                                                                                                                                                                                                                             SGRAL----GIFEPVEYKNYLLVDGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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0.0016;
---- 72; Indels
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
GSZ protein (DXS1283E).
          Similarity 27.6%; Pred. No. 0.001
58; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            160 VNNLPVEPPQESGIPTVCVDVLPIEPEXDI 189
                                                                                                                                                                                                                                                                                                                                                                                                         171 SDNOPI ----TVTVSPFSGESDI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: TO C.ELEGANS C05D11.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U03886; AAA16491.1; -.
EMBL; U0888; AAA17838.1; J.
EMBL; U08889; AAA17838.1; JOINED.
EMBL; U08899; AAA17838.1; JOINED.
EMBL; U08891; AAA17838.1; JOINED.
EMBL; U08891; AAA17838.1; JOINED.
EMBL; U08891; AAA17838.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
MEDLINE=95104848; PubMed=7806223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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     Best Local Similarity
Matches 58; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GS2 HUMAN
                                                                                                                                                                                                                                                                             119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                67 - KRVNWIKLFKFKPPLKGLI------GW-----EKAIRFLEEVL---PYRRIEK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 IVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGMFSIL---- 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 LEIPTYLCATDLYSGRAL--YLSEGSLI-PALLGSCAIPGIF--EPVEYK-----
                                                                                                                                                                                                                                                                                                                                                       Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI TaxID=6239;
                                                                                                                                                                                                                                                                                                    10.4%; Score 132.5; DB 1; Length 910;
llarity 30.4%; Pred. No. 0.00045;
Conservative 22; Mismatches 75; Indels 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO HUMAN GS2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Du \mathbf{Z} , submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                     910 AA; 102716 MW; 1CFC03C4A6E64B9C CRC64;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein CO5D11.7 in chromosome III.
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                                                                                                                                                                                                        POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             +61 TGSSSVKFVDGSVDNDLPISRLSE 484
                                                                                                                                                      Hypothetical protein; Transmembrane.
TRANSMEM 282 302 POTENTI
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                                  PIR; S38167; S38167.
PIR; S39130; S39130.
SGD; S0001797; YKR089C.
InterPro; IPR002641; Patatin.
Pfam; PF01734; Pátatin; 1.
             EMBL; Z28314; CAA82168.1;
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62; Conserv
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Q11186;
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YPD7 CAEEL
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"Analysis of the Escherichia coli genome VI: DNA sequence region from 92.8 through 100 minutes.";
Nucleic Acids Res. 23:2105-2119(1995).
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Hypothetical protein; Complete proteome.
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MEDLINE=95334362; PubMed='
Burland V.D., Plunkett G.
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                                                                                                                                                                                                                                                              LRLRKFE--EINLYLSGGAAKGIAHIGYLKAINELGIRVRA-----LSGVSAGA-IVS
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---LQMDTAARLFDSGKSFYMCACRQDDYAPNYFLPTKQNWLDVIRASSAIPGFYRSGVSL
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hett G. III, Sofia H.J., Daniels D.L.,
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-!- COFACTOR: FAD (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE ETF-QO / FIXC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Nucleotide sequence of the fixABC region of Azorhizobium ORS571: similarity of the fixB product with eukaryotic flatcharacterization of fixX, and identification of nifW."; Mol. Gen. Genet. 225:514-520(1991).

-I- FUNCTION: COULD BE REQUIRED FOR THE FORMATION OF A FUN NUTROCENAGE FOR PROFEIN: PROBABLY ACCEPTS ELECTRONS FROM NUTROCENAGE FOR THE PROBABLY ACCEPTS ELECTRONS FROM NUTROCENAGE FOR THE PROBABLY ACCEPTS ELECTRONS FROM NUTROCENAGE FOR THE PROBABLY ACCEPTS ELECTRONS FROM NUTROCENAGE FOR THE PROBABLY ACCEPTS ELECTRONS FROM NUTROCENAGE FOR THE PROBABLY ACCEPTS ELECTRONS FROM NUTROCENAGE FOR THE PROBABLY ACCEPTS ELECTRONS FROM NUTROCENAGE FOR THE PROBABLY ACCEPTS ELECTRONS FROM NUTROCENAGE FOR THE PROBABLY ACCEPTS ELECTRONS FROM NUTROCENAGE FOR THE PROBABLY ACCEPTS ELECTRONS FROM NUTROCENAGE FOR THE PROBABLY ACCEPTS ELECTRONS FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAGE FROM NUTROCENAG
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                            TVCVDVLPIBPBKDIKNILHILLRSFFLAV-RSNSEKRKEFCDLVIVPELEE
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--LKDMKKYKDLPALLHINSQNFFLTYPQLVSKAMQNFVRVDGTPKVEK
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23, Last sequences, 35, Last annotations.
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48578 MW;
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28 FAD OR NAD(P) (ADP PART)
48578 MW; A736998BDFAE34E2 CRC64;
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Result	Score	Query Match	% Query Match Length DB	DB	ID	Description
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7	289	22.7	760	16	QBR6F6	
80	287.5	22.6	304	ν	Q93KA7	ወ
9	285.5	22.4	491	N	Q93CN4	Q93cn4 bacteroides
10	284.5	22.3	303	N	086196	O86196 pectobacter
. 11	284.5	22.3	321	16	Q92QB6	Q92qb6 rhizobium m
12	279	21.9	286	N	Q9RA24	Q9ra24 vibrio mari
13	276	21.7	293	16	Q8YB65	Q8yb65 brucella me
14	274.5	21.6	300	16	Q9JWV3	Q9jwv3 neisseria m
15	273	21.4	314	16	96HX8Ö	
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124	65 EMLKLLKEVNWLKLFKFKTPKMGLMGWEKAAEFLEKELGVKRLEDLNIPTYLCSADLYTG 124		D	
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120	61 GMFSLLKRVNWLKLFKFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICATDLYSG 120		Ó	
64	5 LKLKRFEEVNLVLSGGAAKGIAHIGVLKALEELGIKVKRLSGVSAGAIVSVFYASGYTPD 64		Дb	
60	BEINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPB		Ş	
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	ller M., Auja	Grahan	ŖΑ	
	Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,	Decker	RΑ	
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	l protein AO 1386.	Hypoth	B	
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                        97 VLPY----RRIEKLBIPTYICATDLYSGRALYLSEGSLIPALLGSCAIPGIFRPVEYKNY 152
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MEDLINE=20437337; PubMed=10984043;
StOVET C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener B.,
Hickey M.J., Brinkman F. S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino B., Westbrock-Madman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E. W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 KIGLVLS(KGARARGLAHIGVLKALDEQCIQIDAIAGTSWGAVVGGLYASGYTPAELERIAL
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                                                                                                                                                                  8 EINLVLS(#GAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGMFSLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Gaps
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Pseudomonas.
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InterPro; IPR002641; Patatin.
Pfam; PF01734; Patatin; 1. #
Hypothetical protein; Complete proteome.
SEQUENCE 728 AA; 80898 MW; CF6A11883D916043 CRC64;
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Last annotation update)
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Nature 406:959-964 (2000)
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124 KEGDLIKAIRASISIPAFFEPVEYNGTKLVDGSIVDSEAIBLAASLGADIIINCDVSSSI 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 SEGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEPFQESGIPTV-----CV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D-----VLPIEPEKDIKNILHILLRSFFLAV---RSNSEKRKBFCD--- 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 DMGFFERFFYSLANSEKVLPIKKYFNIKRPLPEIISITTTÄIKLLKDNSNKNLEKMEGNK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 INLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGMFSLLKR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acide Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35; Gaps
                                                                                                                                                                                                                                   DB 16; Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
NCPI_TaxID=86665;
01-JUN-2002 (TIEMBLRel. 21, Created)
01-JUN-2002 (TIEMBLRel. 21, Last sequence update)
01-JUN-2002 (TIEMBLRel. 21, Last annotation update)
Predicted esterase of the alpha-beta hydrolase superfamily.
RSSA OR TTE1838.
                                                                                                                                                                                                                                                                                                                                                                                                                                         25.3%; Score 322.5; DB 16; Length 2 31.2%; Pred. No. 3.4e-21; ive 48; Mismatches 107; Indels
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SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE-20512562; Pubmed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., M.
Puji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
UJUM-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein BH2587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 --LVIVPELEEFTPLDVRKADQIMERGYIKALEVLS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 RVYTIKPNVDNIRWYRFDQAEKCINMGFEAADSIVA 279
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Best Local
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01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Grmolaeva M.D., Vanathevan J., Bass S., Qin H., Dragoi I., Sellers P.

McDonald L., Utterback T., Fleischmann R.D., Nierman M.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical provided vice vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01237; UPP0028; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 275 AA; 30545 MW; 617C790E9E4E7553 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9KUB9
                                                                                                                                                                                                                                                                                             Pfán, PFÓ1734; Patatin; 1.
PROSITE; PSO0339; AA TRNA LIGASE II 2; UNKNOWN 1.
Hypothetical protein; Complete proteome.
SEQUENCE 764 AA; 85616 MW; 0C3CC8BCA100C840 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. SEROTYPE O1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE004145; AAF93770.1; -. TIGR; VC0603; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002641; Patatin.
InterPro; IPR001423; UPF0028.
Pfam; PF01734; Patatin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002106; AAtRNA ligaseII.
InterPro; IPR002641; Patatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 406:477-483 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "DNA sequence of both chromosomes of the cholera pathogen Vibrio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125
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MFSLLKRVNWLKLFK---
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                                                                               QVAKRPKĪALVLAGGGĀKGĀĀHMGVLRĀLBĒMHVPVDIITGTSMGĀYVGGLYĀTGMSĀBĒ
                                                                                                              RLRKFEBINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) (TrEMBLrel. 15, 0) (TrEMBLrel. 15, 12 (TrEMBLrel. 21, 12 (TrEMBLrel. 21, 13) protein VC0603.
                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                      23.4%;
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                                                                                                                                                                                    61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                       Score 297.5; DB 16;
Pred. No. 2.2e-18;
1; Mismatches 105;
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                        --FKPPLKGLIGWEKA 90
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RESULT 6
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Matches 84
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Q8Y066;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21681879; PubMed=11823852;
Salanoubat M., Genin S., Artiguerave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415;497-502 (2002).
Tattopro: TEDEOCACIA 1880.1;
TENEDOCACIA 1880.1;
TENEDOCACIA 1880.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome
SEQUENCE 319 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rropable lipoprotein transmembrane.
RSC1178 OR RSO4543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=GMI1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002641; Patatin.
Pfam; PF01734; Patatin; 1.
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                              235
                                                                                                                                                                    121
285
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                                                                                                                                                                                                      113 MDEATIADWALPFGTRFGGWLKG----BALEKYVNRLVKQKTIEQMRIPLGIVATDLGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRFLEEV---LP-YRRIEKLEIPTYICATDLYSGRALYLSEGSLIPALLGSCAIPGIFEP 146
                                                                                                                                                                                                                                      R-----VNWLKLF--KFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICATDLYSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEYKNYLLVDGGIVNNLPVEPFQESGIP-TVCVDV-LPIBPEKDIKNILHILLRSFFLAV 204
                              DQIM--ERGYIKALEVLSE
                                                                                                LPIEPE-KDIKNILHILLRSFFLAVRSNSEKRKEFCDLVIVPEL----EEFTPLDVRKA 234
                                                                                                                                                   RALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLYDGGIVNNLPVEPFQESGIPTVCVDV 180
                                                                                                                                                                                                                                                                                                       INLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSP-EGMFSLLK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRSTERQSDHLTSRDLLLRPPVGKMETMEFDKMPAAFAMGYQEAMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSNSEKRKEFC---DLVIVPELEEFTPLDVRKADQIMERGYIKALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEIDGLWLVDGGVTNNMPVEVARAMGADIIIAVDISTDYKSQEDFTNLFTVADQLSNYLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEALIYSVDWNRGYRDRVDRSQRRVRDKEYEDRYQITTDLGLHW(;EVRAP-KGVVQGQNM
EAILGGEQAALAAMPLLRE
                                                                ISADPSAQAVSGQASMLLQTTTIMGQSINKTELAQADVVIAPSLPFVKGSDFT----ARN
                                                                                                                                                                                                                                                                       IGLALGGGAARGFAHIGVIKALEAQGIQIDFITGTSAGSVVAALYASGMSGIELNRQALK 112
                                                                                                                                    RPILFRRGNTGQAVRASCSIPGVFQPVTISGHQYVDGGLVAPVPVTYAKQMGATFVIAVN
                                                                                                                                                                                                                                                                                                                                                                                                             319 AA; 32967 MW; 6924B744D4F53342 CRC64;
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                         23.1%; Score 294; DB 16; 32.4%; Pred. No. 1.5e-18; tive 51; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                251
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                                                                                                                                                                                                                                                                                                                                           100;
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312
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                                                                                                                                                                                                                                                                                                                                                                             319;
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                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT Q8R6F6

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69 VNWLKLFKFKPPLK------GLIGWEKAIRPLEEVLPYRRIEKLEIPTYICATDLYS 119
                                                                                                                                                                                                                                                                                                                                             120 GRALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLLVDGGIVNNLPVEPFQESGIPTVCVD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 KSEDFKRWYSGEVEEKYMYYFKGNLPTPEFFNIRFSFKDSLSLKPQFLPTSVVNPIQMNL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 ----YRR-----IEKLBIPTYICATDLYSGRALYLSEGSLIPALLGSCAIPGIFEP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 VEYKONYLLVDGGIVNNLPVEPPQESGIPTVCV-DVLPIEPEKDIKNILHILLRSFPLAVR 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 OKVGLVLSGGGAKGLTHIGIIRALEENNIPIDYIIGTSMGAIVGSLYAMGYSPDDMRTLL 85
                                                                                                                                                                                            9 INLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGMFSLLKR 68
                                                                                                                                                                                                                           9 IGLALGSGAAKGWAHIGVLKALEDLGIVPDVVAGCSVGALVGAAYAT------HRLDSM 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 RSFFLAVRSNSEKRKEFC----DLVIVPELEEFTPLDVRKADQIMERGYI----KALBVL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 MSTSIQILENKLKAARMAGDPPDVIJQPYCPQIATLDFHRAEEAIESGRLAVEKQLELL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 KRVNWLK-------LIGKFKPPLKG------99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smalley D., Smith C.J.;
An Aerobic-Type Ribonucleotide Reductase in the Anaerobe Bacteroides
fragilis.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 BEINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGMFSLL
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; CFB group; Bacteroidetes; Bacteroidales; Bacteroidaceae; Bacteroides. NCBI_TaxID=817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.4%; Score 285.5; DB 2; Length 491; 25.7%; Pred. No. 1.5e-17; ive 63; Mismatches 105; Indels 43;
                                                                                   Length 304;
                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER 491 491
SEQÜENCE 491 AA; 56622 MW; 28ACDE4AE030A4AD CRC64;
Pfam; PF01734; Patatin; 1.
SEQUENCE 304 AA; 33490 MW; CPC28B590E24BB4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 19, Last sequence update)
Hypothetical 56.6 kDa protein (Fragment).
Bacteroides fragilis.
                                                                             22.6%; Score 287.5; DB 2; 27.1%; Pred. No. 5.5e-18; ive 50; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 VLPIEPEKDIKNILHILL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF404759; AALO2104.1; -...
InterPro; IPR002641; Patatin.
Pfan; PF01734; Patatin; 1.
Hypothetical protein.
NON_TER 491 491
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Matches 73; Conservative
                                                                                                                                        81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                             Query Match
Best Local Similarity
Matches 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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093CN4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 DVNVSNFLETITDNTNLSLEKKESLKKYSVHLSPDNELNPSFPKGLRGTGEAYLLLKGLL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -PYRRIEKLE---IPTYICATDLYSGRALYLSEGSLIPALLGSCAIPGIFEPVEYKNYLL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 VDGLVSRNLPVEEAYEMGADIVVASDIGAPVVEKDDYNILSVNNQASTIQASNITKISRE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDGGIVNNLPVEPPQESGIP-TVCVDVLPIEPEXDIKNILHILLRSFFLAVRSNSEKRKE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 EINLVLSGGAAKGIAHIGVLKAINELGIRVRALSGVSAGAIVSVFYASGYSPEGMFSLLK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 RV---NWLK------LFKFKPPL-----KGLIGWEKAIRFLEBVL 98
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-21886394; PubMed=11889109;

Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,

Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,

Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,

A grome sequence and analysis of the oral bacterium Fusobacterium

nucleatum strain ATCC 2586.",

J. Bacteriol. 184:2005-2018(2002).

RMBL; AEO10475; Alle3819.1; --.

RMBL; AEO10475; Alle3819.1; --.

Protease; Hydrolase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.7%; Score 289; DB 16; Length 760;
29.4%; Pred. No. 1.3e-17;
tive 54; Mismatches 104; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            control of
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Pectobacterium.
NCBI_TaxID=556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBirel. 21, Created)
01-JUN-2002 (TrEMBirel. 21, Last sequence update)
01-JUN-2002 (TrEMBirel. 21, Last amnotation update)
Serine protease (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 FCDLVIVPELEEFTPLDVRKADQIMERGYIKA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 KASILISPDVKNISALDSSKKEELMKLGKVAA 333
760 AA.
                                                                                                                                                                                      Pusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterium.
NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 29.48 tes 80; Conservative
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A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC A PAC 
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SNSEKRKEFCDLVIVPELEEFTPLDVRKADQIMERGYIKALEVL

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RESULT 10
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RESULT
Q92QB6
ID Q9
DT 011
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"The response regulator ExpM is essential for the virulence carotovora subsp. carotovora and acts negatively on the sign
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Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591787; CAC45597.1; -.
InterPro; IPR002641; Patatin.
Pfam; PF01734; Patatin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batu Capela D., Becker A., Boutry M., Cadleu E., Dreano S., Glous Boistard P., Becker A., Boutry M., Cadleu E., Dreano S., Glous Bootnie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                       Genes, similar to eicosapentaenoic acid Vibrio marinus (Moritella marina).
                                                                                                                                                                                                                                                                                                                               Q9RA24;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21396507; PubMed=11481430;
                                                                                                                                                                                                                                                Moritella
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                                                                   InterPro;
Pfam; PF01
                                                                                             docosaĥexaenoic acid-producing bacterium Vibrio Biotechnol. Lett. 21:939-945(1999).
                                                                                                                                   Tanaka M., Ueno A., Kawasaki K., Yumoto I., Ohgiya S., Hos
Ishizaki K., Okuyama H., Morita N.;
"Isolation of clustered genes that are notably homologous
eicosapentaenoic acid biosynthesis gene cluster from the
                                                                                                                                                                                          STRAIN-MP-1;
                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
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                                                    Pro; IPR002641; Patatin.
PF01734; Patatin; 1.
NCE 286 AA; 31527 MW;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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34380 MW; D9AD7590B84D709F CRC64;
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                                                      31527 MW;
              21.9%;
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Pred. No. 1.1e
47; Mismatches
 Score 279; DB 2
Pred. No. 3e-17;
2; Mismatches 1
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                                                      AAF729C1D2CFE6C9 CRC64;
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                            Length 286
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STRAIN=16M / ATCC 23456 / BIOTYPE 1;
MEDLINE=20020109; Pubmed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis (serogroup A).
Bacteria, Proteobacteria, beta subdivision, Neisseriaceae, Neisseria.
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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MEDLINE=20222556; PubMed=10761919;
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EMBL, AL162752, CAB83536.1; -.

InterPro; IPR002641; Patatin.

Pfam; PF01734; Patatin; 1.

Lipoprotein; Complete protecome.

SEQUENCE 300 AA, 31367 MW; E
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31.8%;
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NCBL_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                             Possible lipoprotein.
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SERAIM-16M / AICC 23456 / BIOTYPE 1;

MEDLINE-20020109; PubMed=11756688;

MEDLINE-20020109; PubMed=11756688;

A Del Vecchio V.G., [Appatral V., Redkar R.J., Patra G., Mujer C., Los T., Del Vecchio V.G., [Appatral V., Redkar R.J., Lykidis A., Reznik G., Jahlonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., A selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., The genome sequence of the facultative intracellular pathogen Broc. Natl. Acad Sci. U.S.A. 99:443-448(2002).

REMBL, ABC09736; AAL5277.1; --

REMBL, ABC07336; AAL5277.1; --

REMBL, ABC01336; AAL5277.1; --

REMBL, ABC01346; AAL5277.1; --

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          LLKRVNWLKLFKFKFPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICATDLYSGRALY 124
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                                                                    67 DVKPFSW----KFTRARAGFIDPAKLYPEVLKYIPEDSFEYLQPELRIVATNMLLGKEHI
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Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group;
Brucellaceae, Brucella.
NCBI_TaxID=29459;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Serine protease (EC 3.4.21.-).
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28.5%; Pred. No. 5.8e-17;
iive 52; Mismatches 99;
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EMBL; AB00953; AAL52089.1; -.
InterPro; IPR002641; Patatin.
Pfam; PP01734; Patatin; 1.
Hydrolase; Complete proteome.
SEQUENCE 314 AA; 34286 MW; E18AADC1225AFDBB CRC64; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen Brucella melitensis.";
61 -----GMFSLLKRVNWLKLFKFKPPLKGLIGWEKAIRFLEEVLPYRRIEKLEIPTYICAT 115
                                                                                                                                                                                                                                                                                                                                    33 QKIALALGGGAARGWAHIGYLRALDBAGIEIEWIAGTSIGALVGGCYLAGKLWELEEFAR 92
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knall gas marine bacterium which grows optimally at 85 deg C and pH 6.8 It can be amplified from a pBluescript vector by FCK (see 6.8 It can be amplified from a pBluescript vector by FCK (see 6.8 It can be amplified from gloundleotides (AAT79321-30) encoding esterases (AAW23069-77, AAW23089) were recovered from genomic gene libraries. They can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases are stable at high temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group from an amino acid to an alpha-keto acid using a claimed esterase. The enzymes may also be useful as ripening starters in cheese making, in lighin removal in paper and pulp manufacture, in carbohydrate derivative synthesis, in the study of plant wall structure, plant lighted for production of highly degradable animal feeds.
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                                                                                                                                                                                                          This DNA sequence codes for thermostable esterase 28LC (AAW23071)
                                                                                          Nucleic acid encoding heat stable esterase from thermophilic
bacteria - which is active in organic solvents, useful in cheese
paper manufacture, and to study plant resistance to disease
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This DNA sequence codes for thermostable esterase VF5-21LC (AAAW23074) of Aquifex VF5, a marine strictly chemolithoautotrophic knall gas bacterium that grows optimally at 85 deg C and pH 6.8.

It can be amplified from a Bluescript vector by PCR (see AAT79312-13). Claimed, newly identified polynucleotides (AAT79321-30) encoding esterases (AAW23069-77, AAW32089) were recovered from genomic libraries. They can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases are stable at high temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino acid to an alpha-keto acid using a claimed esterase. The enzymes CCTGAGCTTGAGGAGTTCACACCCCTTGATGTTAGAAAAGCGGACCAAATAATGGAGAGG 541 CITCCCATAGAGCCGGAAAAGGATATAAAGAACATTCTTCACATCCTTTTGAGGAGCTTC ŏ Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese paper manufacture, and to study plant resistance to disease Baterase; thermostable enzyme; ester; chiral compound; cheese; pulp; paper; lignin removal; sugar; lignocellulose; disease resistance; feedstuff; ss. /transl except= (pos: 295..297, aa:Glu) Maffia AM, Murphy D; 7, Warren PV; 721 GGATACATAAAAGGCCTTAGAGTGACTTTCTGAATAG 756 GGATACATAAAGGCCTTAGAGGTACTTTCTGAATAG 756 DNA encoding Aquifex esterase VF5-34LC (RECO-) RECOMBINANT BIOCATALYSIS INC. Claim 1; Page 48-49; 113pp; English. Link S, Ma. Swanson RV, Location/Qualifiers AAT79327 standard; DNA; 750 BP 97WO-US02039. 96US-0602359 16-FEB-1998 (first entry) , Kosmotka A, Robertson DE, Aquifex sp. strain VF5. WPI; 1997-425035/39. P-PSDB; AAW23074 11-PEB-1997; 16-FEB-1996; WO9730160-A1 21-AUG-1997. Callen W, AAT79327; 601 661 721 Reid J, AAT79327 a ద 셤 셤 Š ð à

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meningitidis;
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72.2%;
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 gonorrhoeae;
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 antigen; vaccine;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequences AAZ11972-Z12358 represent open reading frames (ORFs) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see AAX3849-Y38944). The antigenic proteins, the fragments, their nucleic acids and antibodies are used for diagnosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from Neisseria meningitidis
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CAAGGGAATGCCGGGCAGGCTGTGCGCGCCGTTCCCCAATGTGTTCCAACCC
                       GAAGGGAGTTTAATCCCCGCACTTCTCGGCAGCTGTGCAATTCCCCGGCATATTTGAACCC
                                               CCCATCAAATTTGCCGCCGTTGCTACTGATTTTGAAACCGGCAAGGCCGTCGCTTTCAAT
                                                              GAGATACCGACGTATATATGCGCGACGGATTTATACCCGGGAAGGGCTCTATACCTCTCG
                                                                                                 GGCGAAAAGCTGCAAAATTACATCAACCGAAAAGTCGGCGGCAGGCGGATTCAGCAGTTT
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Pred. No. 5.2e-07;
D; Mismatches 264
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of infection
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199 AAGAGGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTGATAGGG 258
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99US-0132068
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Rappuoli R, Pizza M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ORFS) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see AAY38499-Y38944). The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                  Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
treatment; Neisseria infection; meningitis; septicaemia; gonorrhea; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 ATTAAGGITTTGAAAGAAAAGGTATTCCTGTGAAGGTGGTTACCGGCACATCGGCAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequences AAZ11972-Z12358 represent open reading frames
                      GITGAGTATAAGAATTACTTGCTCGTTGACGGAGGTATAGTTAACAACCTTCCCGT
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                                                                                                                                                                                                      Neisseria meningitidis complete ORF137 sequence
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                                                                                                              AAZ12213 standard; DNA; 903 BP.
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97GB-0023516.
97GB-0024190.
97GB-0024386.
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences, AAA81260 to AAA81303 and AAA82520 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81312 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA8132 to AAA81452 represent Neisseria meningitidis MenB polymucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379 GAAGGGAGTITAATCCCCGCACTICTCGGCAGCTGTGCAATTCCCCGGCATATTTGAACCC 438
310 GAAATTTTAGGCAAAACCGATTTGGTCGATTTAACCTTGTCCACCAGTGGTTTTATCAAA 369
                                                                                                                                                                                                                                                                                319 GAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTG 378
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                                                                                                                                                                                       370 gecgaaaaccrecaaaarracarcaaccgaaaagregeegeeagearreagearrr
                                                                                                   259 TGGGAGAAGGCTATAAGATTCCTTGAGGAAGTTCTCCCTTACAGGAGAATAGAAAAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTGAGTATAAGAATTACTTGCTCGTTGACGGAGGTATAGTTAACAACCTTCCCGT
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Ratti G, Scarselli M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N. meningitidis partial DNA sequence gnm_21 SEQ ID NO:21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have falled mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and
                                                                                                                                                                                                     Neisseria meningitidis B nucleotide sequence SEQ ID NO:114.
                                                                                                                                                                                                                                                                                                           AAF21613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 92934 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which are not antigenically variable or at least more conserved than other more variable regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes,
                                                                                                                                                                                                                                       13-MAR-2001
                                                                                                                                                  diagnosis;
                                                                                                   Neisseria meningitidis
                                                                                                                                                                     Neisseria
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                                                                                                                                                                                                                                                                                                           standard; DNA; 172325
                                                                                                                                                                                                                                                                                                                                                                                                                             GTTGAGTATAAGAATTACTTGCTCGTTGACGGAGGTATAGTTAACAACCTTCCCGT
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                                                                                                                                                   meningitidis; Neisseria gonorrheae;
; antigen; detection; infection; gen
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                                                                                                                                                                                                                                       (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.9%;
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                                                                                                                                                   gene
                                                                                                                                                     immunogenic; vaccine;
e therapy; antibacterial;
                                                                                                                                                   therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 92934;
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08-MAR-2000; 2000WO-US05928

GAAGGGAGTTTAATCCCCGCACTTCTCGGCAGCTGTGCAATTCCCCGGCATATTTGAACCC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences which overlap each other at the beginning and end of each consequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of AAF21607, the last 49980 bp of AAF21507 are repeated at the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the CR Reisseria proteins given in AABS8550 to AABS8593, and AAF21588 to AAF21588 to AAF21606 represent FCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. CR eisseria nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or as a diagnostic reagent for detecting the CR presence of Neisserial bacteria or as a diagnostic reagent endium or computer bacteria. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes the full length genome of Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-1999;
08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis B full length frames are used to detect, treat and
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  CCCATCAAATTTGCCGCCGTTGCTACTGATTTTGAAACCGGCAAGGCCGTCGCTTTCAAT 153441
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                                                                                                                                                     GANATTTTAGGCANAACCGATTTGGTCGATTTAACCTTGTCCACCAGTGGTTTTATCAAA 153561
                                                                                                                                                                                            AAGAGGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTGATAGGG
                                                                                                                                                                                                                                                                      GCAATCGTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAAGGGATGTTCAGCCTTCTG
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                                      GAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCG
                                                                            TGGGAGAAGGCTATAAGATTCCTTGAGGAAGTTCTCCCTTACAGGAGAATAGAAAAACTT 318
                                                                                                                                                                                                                                TCGATTGTCGGCAGCCTTTTTGCATCGGGTATGTCGCCCGACCGCCTCGAATTGGAAGCC
                                                                                                                                                                                                                                                                                                                                               TTGAAAGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTAAGCGGGGGTGAGCGCCGGG 138
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C, Mora M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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99WO-US23573.
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Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 52; DB :
Pred. No. 3e-09
0; Mismatches
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, Scarselli M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome sequence and open readi
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Scarlato V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 172325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40205 T;
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Rappuoli R;
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Sequence 837096 BP; 207534 A; 227065 C; 205215 G; 197280 T; 2 other;

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The present invention describes methods of obtaining immunogenic proteins from Neiseria genomic sequences. AAA81453 to AAA82414

proteins from Neiseria genomic sequences. AAA81453 to AAA82414

cepresent specifically claimed Neiseria meningitidis genomic DNA sequences; AAA81260 to AAA81261 to AAA81263 to AAA81264 to AAA81269 and AAA81304 to AAA81221 represent PCR primers used in the isolation of Neiseria meningitidis DNA sequences; and AAA8122 to AAA81259 and AAA81304 to AAA81221 represent PCR primers used in the cash protein sequences; and AAA8132 to AAA81452 represent Neiseria meningitidis MenB polymucleotide ORF sequences, which are all used in the exemplification of the present invention. The mucleic acid sequences protein sequences, and antibodies against them, can be used as a medicament (or in the manufacture of a composition can be used as a medicament (or in the manufacture of a composition can be used as a medicament (or in the manufacture of a composition be used as a medicament (or in the manufacture of a composition be used as a medicament (or in the manufacture of a composition by a pational some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenia Neiseariae. Identification of sequences conserved matigenic variability. The provision of further, complete sequence may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than conserved than more variable regions.
153440 CAGGGGAATGCCGGGCAGCTGTGCGCGTTCCGCCGTTCCCAATGTTCCAACCC 153381
                                                                                  153380 GTTATCATCGGCAGCATACATATGTTGACGGCGGTCTGTCGCAGCCCGTGCCCGT 153325
                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic;
antigen; vaccine; diagnosis; infection; antibacterial; identification;
Meningococcus B; MenB; ds.
                                                            GTTGAGTATAAGAATTACTTGCTTGACGGAGGTATAGTTAACAACCTTCCCGT 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorthoea
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Ratti G, Scarselli M,
                                                                                                                                                                                                                                                                                                                                   meningitidis partial DNA sequence gnm_37 SEQ ID NO:37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 629-865; 1760pp; English.
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C, Mora M,
                                                                                                                                                                                                            AAA81489 standard; DNA; 837096 BP.
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Rappuoli R, Pizza M;
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                                                                                                                                                                                                                                                                               79 TTGAAAGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTAAGCGGGGGTGAGCGCCGGG
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                                                                                                                                    19 GAAGAGATAAACCTCGTTCTTTCGGGAGGAGGTGCAAAGGGCATAGCCCACATAGGTGTT
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Score 52; DB 21; Length 83
Pred. No. 7.1e-05;
0; Mismatches 265; Indels
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23-AUG-2000; 2000US-0649167.
   Query Match 6.9%;
Best Local Similarity 44.3%;
Matches 211; Conservative (
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polymucleotide (I) and CC polymerase (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CP plymucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating artibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) as polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC diagnostics, forensics, gene mapping, identification or biological activity. CC The polypeptide and polypucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Specification, but was obtained in electronic format directly from WIPO CC at fig. wipo.int/pub/published_pct_sequences.
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Best Local :
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01-SEP-1998;
06-NOV-1997;
14-NOV-1997;
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                                                                                              09-OCT-1998;
                                                                                                                                                20-MAY-1999
                                                                                                                                                                                                                                                                                                             Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
                                                                                                                                                                                                                                                                                                                                                          Neisseria gonorrhoeae complete ORF137 sequence
                                                                                                                                                                                                                                                                                                                                                                                                            08-OCT-1999
                                                                                                                                                                                                                                                                                         treatment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATATTGTGATAGCGGTTGACCTGC
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                                                                                                                                                                                                                                       gonorrhoeae
                                                                                                                                                                                                                                                                                         Neisseria infection; meningitis; septicaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
98GB-0019016.
97GB-0023516.
97GB-0024190.
                                                                                              98WO-IB01665
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Pred. No. 1.4e-05;
0; Mismatches 97;
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                        AAV81946 standard;
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Query Match
Best Local
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27-NOV-1997;
10-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequences AAZ11972-Z12358 represent open reading frames (ORFs) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see AAX3849)-Y38944). The antigenic proteins, fragments, their nucleic acids and antibodies are used for diagnost prevention (as vaccines) or treatment of Neisseria infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteins from Neisseria meningitidis and N. gonorrhoeae diagnosis, treatment and prevention of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are usefu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 GAAGAGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCATAGCCCCACATAGGTGTT
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                                                                                                                                                           GAAGGGAGTTTAATCCCCGCACTTCTCGGCAGCTGTGCAATTCCCCGGCATATTTGAACCC
                                                                                                                                                                                                                                                                               GAGATTTTAGGTAAAACCGATTTAGTCGATTTAACCTTGTCCACCAGTGGTTTTATCAAA
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                                        GTCATCATCGGCAGGCACAAATATGTTGACGGCGGTCTGTCGCAGCCCGTGCCCGTCAGT
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97GB-0025158.
97GB-0026147.
98GB-0000759.
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Pred. No. 5.9e-05;
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DNA; 40138

Sequence 40138 BP; 11845 A; 7635 C; 8758 G; 11900 T; 0 other;

g

WPI; 1999-070271/06.

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Polyketide-like synthesis, PKS; PKS-like gene; PUPA; DHA; transgenic; poly-unsaturated fatty acid; eicosapentenoic acid; docosahexanoic acid; EPA; oil; dietary supplement; infant feeeding formulation; malnutrition; intravenous feeding formulation; cooking oil; fat; anti-inflammatory; cholesterol; open reading frame; ORF; 88.
                                                                           V. marinus PKS-like cluster comprising ORFs 6,7,8 and 9.
                                                                                                                                                                                                                                                                                   Location/Qualifiers
17394..25352
                                                                                                                                                                                                                                                                                                                                            product= "ORF 6"
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/product= "ORF 9"
                                                                                                                                                                                                                                                                                                                                                                                                       product= "ORF 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product= "ORF 8"
                                                                                                                                                                                                                                                                                                                                                                    25509..28160
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                                                                                                                                                                                                                                           Vibrio marinus.
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AAV81946;
                                                                                                                                                                                                                                                                                   Key
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97US-0048650 04-JUN-1997;

(CALJ) CALGENE LLC.

Metz JG;

Facciotti D, Lassner M,

New nucleic acid encoding polyketide-like synthesis enzymes of Vibrio marinus - and transformed plants and microbes that produce polyunsaturated fatty acids, useful as pharmaceuticals and food supplements

Example 1; Fig 5; 153pp; English.

The invention provides polyketide-like synthesis (PKS)-like genes that
are used for the production of long chain poly-unsaturated fatty acid
(PURA) productions. Genes responsible for eicosapentenoic acid (BRA)
production in Shewanella putrefaciens and novel genes associated with the
production of docosabexanoic acid (BRA) in Vibrio marinus are used to
production of docosabexanoic acid (BRA) in Vibrio marinus are used to
generate transgenic plants that can express transgenes encoding PKS-like
generate transgenic plants that can express transgenes encoding PKS-like
genes associated with PURA production. The PKS-like genes are used to
transform plants and microbial cells to give recombinants having altered
contents of PURA (specifically DHA and BRA). Oils from these plants are
useful as dietary supplements (in infant feeding formulations) to give a
VURA profile closer to that of human milk; for treating malnutrition, in
intravenous feeding formulations; in cooking oils, fats etc.), also as
anti-inflammancry agents and for reducing cholesterol levels. Fragments
Cfrom the genes are useful as probes to isolate related molecules or to
detect organisms that express PKS-like genes. The method facilitates
cfrom the genes are useful as probes to isolate related molecules or to
detect organisms that expression in microbes also allows simple
cspaticular PURA profile. Expression in microbes also allows simple
crecovery and control of PURA profile and is not subject to excernal
cvariables such as weather or food supply. The present sequence represents
cm approximately 40 kb PKS-like cluster DNA fragment from V. marinus
comprising open reading frames (ORFS) 6, 7, 8 and 9.

This invention describes novel DNA sequences encoding for polyketide and Schizochtrium. The nucleic acids are useful for isolating related molecules or in methods to detect organisms expressing the PKS-like genes. They are also useful for creating transgenic plants that express poly-unsaturated long chain fatty acids. The poly-unsaturated long chain fatty acids. The poly-unsaturated long chain patients undergoing intravenous feeding or for preventing or treating malnutrition. The poly-unsaturated long chain fatty acids produced recombinantly are useful as dietary supplements for patients undergoing intravenous feeding or for preventing or treating malnutrition. The poly-unsaturated long chain fatty acids can also be incorporated into cooking oils, fats or margarine formulated so that in normal use the recipient receives a desired amount of poly-unsaturated long chain fatty acids. The nucleic acids are also useful in large scale

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                                                              82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA sequences encoding for polyketide (PK)-like synthesis pathway genes from Shewanella, Vibrio and Schizochtrium, useful for creating transgenic plants that express poly-unsaturated long chain fatty acids
                                                                                     14817 AAAİTGGCTİAGİCCİTİTCIGGCGGTGGTGCGAAAGGIAİTGCTCATCITGGTGİTGİTAA
                                                                                                                                         14877 AATACCIGTTAGAGCAAGATATAAGACCGAATGTAATTGCGGGGTACAAGTGCTGGCTCTA
                                                                                                                                                                    143 TCGTTTCGGTCTTTATGCCTCAGGCTACTCCCCTGAAGGGATGTTCAGCCTTCTGAAGA
                                                           23 AGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCATAGCCCACATAGGTGTTTTGA
                                                                                                               83 AAGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTTAAGCGGGGTGAGCGCCGGGGCAA
                                    Gaps
        Length 40138;
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                                   Indels

    W. marinus PKS-like gene cluster encoding ORF6 to ORF9.

     Score 46.2; DB 20;
Pred. No. 0.0012;
0; Mismatches 88;
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     6.1%;
ilarity 52.9%;
Conservative
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Query Match
Best Local Similarity
Matches 99; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         production of docosahexenoic acid and eicosapentenoic acid, and for the modification of the fatty acid profile of host cells and edible plant tissues and/or plant parts. Transgenic production of polyunsaturated fatty acids in particular host cells allows quicker purification from natural sources such as fish or plants. This sequence represents a vibrio marinus DNA fragment encoding the PKS gene cluster incorporating
                                        The present invention provides a DNA sequence encoding an icosapentaenoic acid-biosynthesising enzyme group-like protein group derived from a microbe having docosahexaenoic acid (DHA) productivity. The gene can be used for the industrial production of DHA. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI64984
    Sequence 41587 BP;
                                                                                                                    Claim 4;
                                                                                                                                                production of
                                                                                                                                                             Gene of a docosahexaenoic acid-producing
                                                                                                                                                                                                                                                    15-DEC-1999;
                                                                                                                                                                                                                                                                                15-DEC-1999;
                                                                                                                                                                                                                                                                                                             26-JUN-2001
                                                                                                                                                                                                                                                                                                                                          JP2001169780-A
                                                                                                                                                                                                                                                                                                                                                                    Moritella marina.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Moritella marina icosapentaenoic acid biosynthesis enzyme DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2001
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                              coding
                                                                                                                                                                                                                                                                                                                                                                                                 Cosapentaenoic acid biosynthesis; docosahexanoic acid productivity.
DHA industrial production; ds.
                                                                                                                                                                                                                       (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                               sequence described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA; 41587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATTGGCTTAGTCCTTTCTGGCGGTGGTGCGAAAGGTATTGCTCATCTTGGTGTATTAA 14876
                                                                                                                   Page 10-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGTAAA
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                                                                                                                                                docosahexaenoic acid
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12323 A; 7885 C; 9126 G; 12253 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.1%;
                                                                                                                68pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                              the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46.2;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                             microbe,
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                              the invention
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Query Match Best Local Similarity

6.**1%;** 52.9**%**;

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genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring global expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, environmental stress or other physiological provocation. Extensive
                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a method of monitoring differential expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 6748; 200pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell relative to expression of same genes in one Bacillus cells, by using substrate containing Bac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-416684/44.
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27-MAR-2001;
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2001US-279526P.
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                                                                                                                                                                                                                                                       81 GACGCTTACAGAAGCGGGGTTCACATTGACTATTTAGCTGGTAGCAGCATGGGTGCATT 140
                                                                                                                                                                                                                                84 AGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTAAGCGGGGGTGAGCGCCCGGGGCAAT 143
                                                                                                                                                                                                                                                                                                                                   263
                                                                                                                                                                                                                                                                                144 CGTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAAGGGATGTTCAGCCTTCTGAAGAG 203
                                                                                                                                                                                                                                                                                                       141 GGTGGCGACTATGTATGGCGTAGGCCATTCGGTTGAAACGATGGAAGTTTTTTGCGAAACA 200
                                                                                                                                                                                                                                                                                                                                                        201 TITCAAACGAAAATAITACIIGGAITIITACAGICTCAAAACAAGGGCIITAITGCIGGACA 260
                                                                                                                                                                                                                                                                                                                                                                                264 GAAGGCTATAAGATTCCTTGAGGAAGTTCTCCCTTACAGGAGAATAGAAAAACTTGAGAT 323
                                                                                                                                                                                                                                                                                                                                                                                                        261 AAAGATTGAAAGCCTCATTCGTTTACTAGCTAAAAGACAAAAGCTGGAGTCGCTTTTTCC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                324 ACCGACGIATATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCGGAAGG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 GCCAGTTCAAGIGGTAGCAACTGATCTTTTAAGTGGCCAAAAAGTGGTGATGTCAAAGGG 380
            equals one gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence tag (GST) used in the method of the invention.
                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                        21 GATTGGACTGGCCCTTGGGTCTGGCGGGCTAGGGCTTTGCCCCACATTGGTGTGTTAAA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               384 GAGTTTAATCCCCGCACTTCTCGGCAGCTGTGCAATTCCCGGCATATTTGAACCCGT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
treatment; Neisseria infection; meningitis; septicaemia; gonorrhea; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381 AGACGTCGSCCAAGGCGGTTCGAGCGATTCCAGGCATTTTTGTTCTTGT 437
                                                                                                                                                                                 24 GATAAACCICGITCITTCGGGAGGAGCTGCAAAGGGCATAGCCCACATAGGTGTTTTGAA
                                                                                                                                                                                                                                                                                                                               204 GGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTGATAGGGTGGGA
                                                                                                                                                            Gaps
 follow-up characterisation is unnecessary, when one spot on an array
                                                                                                                                                             0;
                                                                                                                                    DB 24; Length 467;
                                                                                                                                  6.1%; Score 45.8; DB 24; Length 4.4%; Pred. No. 0.00014; ve 0; Mismatches 232; Indels
                                                                                                         Sequence 467 BP; 122 A; 88 C; 133 G; 124 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis partial ORF137 sequence
                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97GB-0023516.
97GB-0024190.
97GB-0024386.
97GB-0025158.
97GB-0026147.
                                                                                                                                               11 Similarity 44.4%;
185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ12212 standard; DNA; 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis
                                                                                                                                            Similarity
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10-DEC-1997;
14-JAN-1998;
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                                                                                                                                                                                                                                                                                              (ORPs) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see AAY38499-Y38944). The antigenic proteins, their fragments, their mucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
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                                                                                                                                      Proteins from Neisseria meningitidis and N. gonorrhoeae useful for diagnosis, treatment and prevention of infection
                                                                                                                                                                                                                                                                          Nucleotide sequences AAZ11972-Z12358 represent open reading frames
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Ratti G, Scarselli M,
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        Scarlato
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     Rappuoli R,
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Galeotti C, Mora M,
  Pizza M,
                                                                                                                                                                                                                      Claim 9; Page 322; 524pp; English.
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99US-0132068
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Best Local Similarity 54.0<sup>5</sup>
***ches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meningococcus B; MenB; ds
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  Masignani
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Rappuoli R, Pizza M;
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                                                      WPI; 1999-327407/27
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30-APR-1999;
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  Grandi G,
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Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -

Disclosure; Page 216; 1760pp; English.

The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 crepresent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAA825620 to AAA81254 to AAA81259 and AAA81304 to AAA81321 represent FCR primers used in the CC AAA81259 and AAA81304 to AAA81321 represent FCR primers used in the CC AAA81259 and AAA81304 to AAA81321 represent FCR primers used in the Sequences; and AAA81322 to CAAA81452 represent Neisseria meningitidis DNA sequences; and AAA81322 to CC AAA81452 represent Neisseria meningitidis DNA sequences, and antibodies invention. The nucleic acid sequences, protein sequences, and antibodies composition can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or dispnosing infection due to CC medicament) for treating, preventing or dispnosing infection due to CC medicament) for treating, preventing or dispnosing infection due to CC Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences and/or against all pathogenic Neissariae. Identification of sequences, and/or against all pathogenic Neissariae in the manufacture of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have also been tried but none have successfully covercome antigenic variability. The provision of further, complete exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions.

Sequence 447 BP; 110 A; 115 C; 114 G; 107 T; 1 other;

Ś 문 б 밁 밁 Query Match 5.6%; Score 42.6; DB 21; Length 447; Best Local Similarity 54.0%; Pred. No. 0.0016; Matches 87; Conservative 0; Mismatches 74; Indels 0 190 250 rcdárrercegcaaccririrrecarcegerarercecceà 290 130 GCAGTGGTCGGTTTGGCACTCGGTGGCGCGCATCTAAAGGATTTGCCCATGTAGGTATT 189 139 GCAATCGTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGA 179 79 TTGAAAGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTAAGCGGGGGTGAGCGCCGGG 138 19 GAAGAGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCATAGCCCACATAGGTGTT 78 ATTAAGGTTTTGAAAGAAAACGGTATTCCTGTGAAGGTGGTTACCGGCACCTCCGCAGGT 0; Gaps 0;

Search completed: June 19, 2003, 13:38:25 Job time: 182 secs

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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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2 US-08-634-642-3
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4 US-09-103-840A-2

4 US-09-103-840A-1

US-08-976-259-71

US-08-326-1178-1

US-08-982-129-1

US-09-178-1768-1

US-09-457-864-1

US-09-328-111-722
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US-08-232-463-14
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Compugen Ltd.
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Sequence 29, Appl
Sequence 305, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 1, Appli
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US-08-602-359A-26
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ALIGNMENTS

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Sequence 26, Application US/08602359A Patent No. 5942430 GENERAL INFORMATION:
                                                                   TELEVAX: 619-678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 NUCLEOTIDE
                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER: IBM PS/2 OPERATING SYSTEM: MS-DOS SOFTWARE: WORD PERFECT 6.0 CURRENT APPLICATION DATA: US/08/602,359A APPLICATION NUMBER: US/08/602,359A
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                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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STATE: CALIFORNIA
                           STRANDEDNESS:
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                                             NUCLEIC ACID
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4225 EXECUTIVE SQUARE, STE 1400
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GENOMIC DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.6%; Score 397.8; DB 2; 72.4%; Pred. No. 3.2e-122; iive 0; Mismatches 197;
SSEE: FISH & RICHARDSON P.C.
1. 4225 EXECUTIVE SQUARE, STE 1400
CALIFORNIA
CALIFORNIA
                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,359
FILING DATE: February 16, 1996
CLASSIFCATION: 435
PRICATION NUMBER: BAPPLICATION DATA:
APPLICATION NUMBER: BAPPLICATION INFORMATION:
NAME: HAILE, ILSA A.
RECISTRATION NUMBER: 38,347
RECISTRATION NUMBER: 38,347
RECISTRATION INPORMATION:
TELLEPAN: 619-678-5070
TELLEPAN: 619-678-5070
TELLEPAN: 619-678-5079
INFORMATION FOR SEG ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 750 NUCLECTIES
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Best Local Similarity 72.4
Matches 516; Conservative
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                                                                            COUNTRY:
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                                                                          1 TTGAGATTGAGGAAATTTGAAGAGATAAACCTCGTTCTTTCGGGAGGAGGTGCAAAGGGC
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                                      Gaps
                                        ;
    Length 756;
                                      0; Indels
Query Match 100.0%; Score 756; DB 2; L. Best Local Similarity 100.0%; Pred. No. 3.7e-241; Matches 756; Conservative 0; Mismatches 0;
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US-08-602-359A-29
Sequence 29, Application US/08602359A
; Patent No. 5942430
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APPLICANT: MARFIA, Anthony
APPLICANT: MARFIA, Anthony
APPLICANT: SWANSON, ROLL
APPLICANT: WARREN, PATRICK V.
APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ALDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROBERTSON, Daniel B
MURPHY, Dennis
REID, John
WAFFIA, Anthony
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APPLICANT: ROBERT
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RESULT 3
US-09-221-017B-305
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                         US-09-221-017B-305
                                                                                                                                                                            TELEX: 706141
TELEX: 706141
INFORMATION FOR SEQ ID NO: 30'
SEQUENCE CHARACTERISTICS:
LENGTH: 2108 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 305, Application US/09221017B Patent No. 6444799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version
CURRINT APPLICATION DATA;
APPLICATION NUMBER: US/09/221,017B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                  ORIGINAL SOURCE
                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 09-APR-1998 PRIOR APPLICATION DATA:
                                                                                                               ANTI-SENSE:
                                                                                                                                          MOLECULE TYPE:
                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                          NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                  NAME/KEY: misc_feature
                                                                                ORGANISM: PORYPHYROMONAS GINGIVALIS
                                        LOCATION:
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N: P. GINGIVALIS NUCLEOTIDES AND USES THEREOFES: 1120
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US-09-090-793-12
US-09-090-793-12
; Sequence 12, Application US/09090793
; Patent No. 6140486
; GENERAL INFORMATION:
    TITLE OF INVENTION: Production of polyunsaturated fatty acids by expr
    TITLE OF INVENTION: of polyketide-like synthesis genes in plants
; FILE REFERENCE: CGNE.131.01US
; CURRENT APPLICATION NUMBER: US/09/090,793
; CURRENT APPLICATION NUMBER: 05/0408,650
EARLIER APPLICATION NUMBER: 60/048,650
EARLIER APPLICATION NUMBER: 60/048,650
EARLIER TILING DATE: 1997-06-04
NUMBER: OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
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Best Local
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Local Similarity
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AGTTCTT 1973
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                                                                    GGTACTT 747
                                                                                                                                             ACCATTCCACGTGGAGCCGGCAGAAGAAATTGCCGCTTTCGGATACNAAATGGCCAAACA 1.966
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Pred. No. 6.6e-21;
0; Mismatches 386; Indels
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                                                                                                                                                                                                                                          3 GAGATTGAGGAAATTTGAAGAGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCAT 62
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APPLICANT: WHITE, Claire M.
APPLICANT: VENTER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCHICASIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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                                                                                               Query Match 5.3%; Score 40.4; DB 1; Length 7218; Best Local Similarity 7.4%; Pred. No. 0.0052; Matches 32; Conservative 206; Mismatches 192; Indels 0
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Best Local Similarity 52.6%; Pred. No. 52;
Matches 70; Conservative 0; Mismatches 63; Indels
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Patent No. 6294238
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
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   ; CLONE: pTZgpt-Fl8
US-.08-232-463-14
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LENGTH: 4403765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14817 AAATTGGCTTAGTCCTTTCTGGCGGTGGTGCGAAAGGTATTGCTCATCTTGGTGTATTAA 14876
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                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                             Length 40138;
                                                                                                                                                                                                         Query Match 6.1%; Score 46.2; DB 3; Length 40
Best Local Similarity 52.9%; Pred. No. 0.00016;
Matches 99; Conservative 0; Mismatches 88; Indels
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PatentIn Release #1.0, Version #1.25
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
NUMBER OF SEQUENCES: 52
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REGISTRATION NIMBER: 29,768
REFERENCE/DOCKTY NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner.
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08232463
Patent. No. 5670367
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (703) 683-4109
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STRANDEDNESS: single
                                                                  TYPE: DNA
CRGANISM: Vibrio marinus
US-09-090-793-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14997 ATGTAAA 15003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 GGGTAAA, 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-232-463-14/c
SEQ ID NO 12
LENGTH: 40138
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Patent No. 6033889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09103840A Patent No. 6294328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FLBISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 4411529
                                                                                                                                                                   APPLICANT: KIM, SUNG HOU
APPLICANT: LIM, JAE HWAN
APPLICANT: RYU, JAE RYSON
APPLICANT: RYU, JAE RYSON
APPLICANT: CHOI, IN GEOL
TITLE OF INVENTION: GENE SEQUENCE OF AQUIFEX PYROPHILUS
TITLE OF INVENTION: SUPEROXIDE DISMUTASE AND PROTEIN EXPRESSED IN ESCHERICHIA
TITLE OF INVENTION: COLI
                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local 5. 70;
                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370748 CTGCCCGAGTTGA 370760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370688 GTGCCGGTGTTGCCGATGCCAACGTTTCCGTTGCCCGAGTTGAAAAAGCCGATGTTTCCG 370747
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                                CITY: ARLINGTON
STATE: VA
                                                                         STREET:
COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464 TTGACGGAGGTATAGTTAACAACCTTCCCGTTGAGCCCTTTCAGGAAAGCGGTATTCCCA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404 TCGGCAGCTGTGCAATTCCCGGCATATTTGAACCCGTTGAGTATAAGAATTACTTGCTCG 463
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                                                                         1755 S.
                  USA
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                                                                                                                                                                                                                                                                                                          YU, GYU YU
                                                                                                            OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.3%;
                                                                         JEFFERSON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32.2;
Pred. No. 52
                                                                         DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52
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                                                              ORGANISM: Homo sapiens
FRATURE:
FRATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6426186 404040.2CB1
NAME/KEY: unsure
LOCATION: 11-13, 15-17, 25, 35, 1273, 1281, 1288, 2402
OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-101
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                                                                                                                                                                                                                                                 SOFTWARE: PERI
SEQ ID NO 101
LENGTH: 2409
TYPE: DNA
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
Query Match 4.1%; Score 31; DB 4; Length 2409; Best Local Similarity 64.8%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael
TITLE OF INVENTION: BONE R
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APPLICATION NUMBER: JP 97-1140
PILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2901-01
                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2057 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 703-413-3000
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 54.9 es 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      493 GTTGAGCCCTTTCAGGAAAGCGGTATTCCCACCGTTTGCGTTGATGTCCTTCC 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              433 GAACCCGTTGAGTATAAGAATTACTTGCTCGTTGACGGAGGTATAGTTAACAACCTTCCC 492
                                                                                                                                                                                                                                                                                                                     PERL Program
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0

46;

Conservative

0

Mismatches

Indels

0;

Gaps

0

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US-08-634-642-3; Sequence 3, Application US/08634642; Patent No. 5879687
                    Sequence 3, Application US/08607509
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LENGTH: 1867 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (206) 682-6031
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Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: sing
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                                             Patent No. 5876735
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY:
; LOCATION:
US-08-607-509-3
                                                                                                                                                                                                                                                            COUNTRY:
US-08-607-509-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 TCCTGACCTGAATGCAGATAAAGGACGTGAGGATCTCCCCACCAGTTGTTCTGAGATCAGC 192
                    46 GGAGCTGCAAAGGGCATAGCTGTTTTGAAAGCTATAAACGAGCTCGGTATA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 cagcrerrireagerearricirirearigeraargecacaargereaarraceeerragagaa 252
                                                           876 GCACCAGCAAAAGCGATTTCCAACATATGTGTTTTGGAGGTAATTAAGTAACTCTGTATA 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           582 CATCCTTTGAGGAGCTTCTTTGCGGTCCGCTCAAACTCCGAAAAGAGAAAGGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               642 TIGIGACCICGITATAGITCCIGAGCTTGAGGAGITCACACCCCTTGATGTTAGAAAAGC
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Pred. No. 4.6;
0; Mismatches 56; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM:
Macintosh 7.5
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/74/574
FILING DATE: No. 6015939ember 7, 1996
CLASSIFICATION ATA:
APPLICATION NUMBER: 60/023,502
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,315
FRIOR APPLICATION NUMBER: 60/006,315
FRIOR APPLICATION NUMBER: 30,996
FRIOR APPLICATION NUMBER: 30,924
ATTOMEY/AGENT INFORMATION:
NAME: Carl J. Schwedler
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
TELEPHONE: (916) 753-6313
TELERPHONE: (916) 753-6313
TELERPHONE: (916) 753-6313
TELERPHONE: CHARACTERISTICS:
TENERMATION FOR ERGID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        Sequence 3, Application US/08747574

Patent No. 6015939

GENERAL INFORMATION:
APPLICANTION:
TITLE OF INVENTION: PLANT VDE GENES AND
TITLE OF INVENTION: METHODS RELATED THERETO
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
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MOLECULE TYPE: CDNA to mRNA
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l Similarity 53.3%;
64; Conservative
                                                                                                        106 AGGGTGAGGGC 116
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Best Local Similarity
Matches 64; Conserv?
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RESULT 11

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APPLICANT: Reed, Steven G.
TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSED: SEED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STRET: Washington
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF
TITLE OF INVENTION: PROTECTIVE IMMUNE RESPONSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Reed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1867 base pairs
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ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 12-DEC-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 18-APR-19
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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COMPUTER READABLE FORM:
TYPE: Floppy disk
                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
            NAME: Maki, David J. REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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REFERENCE/DOCKET NUMBER:
                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                  CITY: Seattle
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                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                Washington
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117..1325
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                                                                                      12-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                       , Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.9%;
48.5%;
                                                                                                                                                                                                                                                                                                                                                                     METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
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                                                                                                  US/08/989,370
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Pred. No. 8
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                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                 246 GGGATTGATAGGGTGGGAGAAGGCTATAAGATTCCTTGAGGAAGTTCTC 294
                                                                                                     186 GTTCAGCCTTCTGAAGAGGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAA 245
                                                                                                                                        641 GGTGCTCGACGACGATGATGAGATGCTGTCTCAGGGCTTCGCGGACCAGATTTACGAGAT 700
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                                                                    CTTCCGCTTCCTGCCGAAGGACATCCAGGTCGCGCTCTTCTCCGCCACGATGCCGGAGGA
GGTACTGGAGCTGACGAAGAAGTTCATGCGCGACCCCGTGCGTATTCTC
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Pred. No. 8
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US-08-602-359A-26/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                   APPLICATION NUMBER: 1
FILING DATE: Februar:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                             CURRENT APPLICATION DATA:
                            TELECOMMUNICATION INFORMATION:
                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
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                                         NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/010001
                                                                                                                                                                                                                                                                                                                               STREET: 4225 EX
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            TELEPHONE:
                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                     CALIFORNIA
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: 619-678-5070
619-678-5099
                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MURPHY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAFFIA, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                          KOSMOTKA,
                                                                                                                                                                                                             WORD PERFECT 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROBERTSON, Daniel E
                                                                                                                                                                                                                                              IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                   FISH & RICHARDSON P.C.
                                                                                                                                                      February 16,
N: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dennis
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                                                                                                                                                                                US/08/602,359A
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Sequence 104, Application US/08961527

Patent No. 6420135

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: ROCAVILLE

STREET: MARYland
                                                                                                                                                                                                                                                                            631 TCTTTTCKGAGTTTGAGCGGACCGCAAGAAGGAGCTCCTCAAAAGGATGTGAAGAATGT 572
                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                       516 TATTCCCACCGTTTGCGTTGATGTCCTTCCCATAGAGCCGGAAAAGGATATAAAGAACAT 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5464 cirrricaararccraaacirroridaadaccaaccaacraageccarcrarcaacrarir 5523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 CTTCTGAAGAGGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTG 252
                                                                                                                                                                                                                                                                                                                                                  576 TCTTCACATCCTTTTGAGGAGCTTCTTTCTTGCGGTCCGCTCAAACTCCGAAAAGA 631
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                                                                                                                                                                  DB 2; Length 756;
                                                                                                                                                             Score 29.6; DB 2; Length 7:
Pred. No. 5.7;
0; Mismatches 54; Indels
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Pred. No. 19;
0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: BTOOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFRERNCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 ATAGGGTGGGAGAAGGCTATAAGA 276
                                                                                                                                                             ch
l Similarity 53.4%;
62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.9%;
Best Local Similarity 59.5%;
Matches 50; Conservative
                                                                                                    GENOMIC DNA
                          756 NUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 6735 base pairs
SEQUENCE CHARACTERISTICS:
LENGTH: 756 NUCLEOTIDE
TYPE: NUCLEIC ACID
                                                               SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                         Query Match
Best Local Similarity
Matches 62; Conserv
                                                                                  LINEAR
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                                                         ; STRANDEDNESS;
; TOPOLOGY: LINI
; MOLECULE TYPE: (
US-08-602-359A-26
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Db 5524 TAAATGAATGGCAAGTTACTAAGA 5547
Search completed: June 19, 2003, 14:22:18
Job time: 64 secs
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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100.0
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
26/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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                                                                                                            9 US-10-027-805-26

9 US-10-027-804-26

10 US-99-903-410-26

9 US-10-027-805-29

9 US-10-027-804-29

10 US-99-903-410-29

10 US-99-974-300-6748

10 US-99-974-300-6748

10 US-99-974-300-2350

9 US-10-295-403-89

9 US-10-184-644-546

9 US-99-925-25-38
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                                                                       US-09-887-576-66
US-09-887-576-184
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_NEW_PUB.seq:*
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Sequence 26, Appl
Sequence 26, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 12, Appl
Sequence 6748, Appl
Sequence 1639, Ap
Sequence 1639, Ap
Sequence 546, Appl
Sequence 546, Appl
Sequence 546, Appl
Sequence 546, Appl
Sequence 546, Appl
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US-10-027-805-26
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30.4	30.6	30.6	30.6	30.6	30.6	30.8	30.8	30.8	30.8	30.8	31	31	31	31	31.4	31.6	31.6	31.6	31.6	31.8	32	32	32	32	32	
4.0	4.0	4.0	4.0	4.0	4.0	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	
407	368004	2781	751	657	442	684973	11928	11928	11928	11928	4138	1622	653	653	7004	1503841	1503841	1503841	378361	476	17569	17569	17569	17569	1332	
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US-09-960-352-2555	US-09-949-654-3	US-10-003-356-9	US-09-974-300-1332	US-10-003-356-3	US-09-933-797-266	US-09-263-959-1	US-10-199-024-58	US-10-199-024-57	US-10-199-024-56	US-10-199-024-55	US-09-802-472B-5	US-09-822-846-407	US-10-184-634-402	US-10-184-644-402	US-10-239-676-119	US-09-795-686-1	US-09-795-668-1	US-09-946-807-1	US-09-901-136-3	US-09-864-761-14535	US-10-017-754-1804	US-09-849-626-1804	US-09-902-941-1804	US-09-736-457-1804	US-09-938-842A-1753	
25	Segmence 3 Appli		13.	œ	66.	е 1	58	57	D	Ğ.	е 51 ~		402	402	19. App	Sequence 1, Appli	e L			e 14535		1804,	1804,	1804.	Sequence 1753, Ap	

ALIGNMENTS

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Sequence 26, Application US/10027805
Patent No. US20020164725A1
GENERAL INFORMATION:
       INFORMATION FOR SEQ ID NO:
COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/027,805
FILING DATE: 21-Dec-2001
CLASSIFICATION: UDATA:
APPLICATION UDATA:
APPLICATION NUMBER: 08/602,359
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: 08/602,359
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION UMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/01000
TELEPHONE: 619-678-5070
TELEPHONE: 619-678-5070
TELEPHONE: 619-678-5070
TELEPAX: 619-678-5099
FORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: LA JOLLA
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 4225 EXECUTIVE SQUARE, STE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWANSON, Ronald V. WARREN, Patrick V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAFFIA, Anthony
LINK, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dennis
                                                                                           09010/010001
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AGCGGGGTGAGCGCCCGGGGCAATCGTTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAGCCCACATAGGTGTTTTGAAAGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGAGAATAGAAAAACTTGAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 AGGGCTCTATACCTCTCGGAAGGGAGTTTAATCCCCGGACTTCTCGGCAGCTGTGCAATT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGATGTTCAGCCTTCTGAAGAGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TTGAGATTGAGGAAATTTGAAGAGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCGGGGGCCGGGGCAATCGTTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGAGAATAGAAAACTTGAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TTGAGATTGAGGAAAFTTTGAAGAGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ATAGCCCACATAGGTGTTTTGAAAGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAAGGGATTGATAGGGTGGGAGAAGGCTATAAGATTCCTTGAGGAAGTTCTCCCTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGATGTTCAGCCTTCTGAAGAGGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 756; DB 9; L
100.0%; Pred. No. 1.9e-247;
tive 0; Mismatches 0;
                                                                                                                                                                                     STREET: 4225 EXECUTIVE SQUARE, STE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REPRENCE/DOCKET NUMBER: 09010/010001
TELECOMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPRAX: 619-678-5099
                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/027,804
PILING DATE: 21.Dec-2001
CLASSIFICATION: <unhombor.<br/>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: GENOMIC DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/602,359
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                            KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON
                                                         SWANSON, Ronald V. WARREN, Patrick V.
       REID, John
MAFFIA, Anthony
LINK, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 26
                                                                                                                                                                                                                                                    ZIP: 92037
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                      CITY: LA JOLLA
STATE: CALIFORNIA
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Best Local Similarity 100.
Matches 756; Conservative
                                                                                                                                                                                                                                         COUNTRY: USA
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                                                                                                                                                             Length 756;
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                                                                                                                                                        100.0%; Score 756; DB 9; L
100.0%; Pred. No. 1.9e-247;
ive 0; Mismatches 0;
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                                                                TOPOLOGY: LINEAR
MOLECULE TYPE: GENOMIC DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
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Publication No. US20030054530A1
GENERAL INFORMATION:
APPLICANT: ROBERTSON, Daniel E.
                LENGTH: 756 NUCLEOTIDES TYPE: NUCLEIC ACID
                                                  STRANDEDNESS: SINGLE
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            Best Local Similarity 100.
Matches 756; Conservative
                                                                                                                    US-10-027-805-26
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240 240 300

180

9

Gaps

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Length 756;

TITLE OF INVENTION. ENZYMES HAVING ESTERASE ACTIVITY AND METHODS OF USE THERBOF FILE REFERENCE: DIVERLIGO-2 CURRENT PILLAGION NUMBER: US/09/903,410 CURRENT APPLICATION NUMBER: US/09/903,410 CURRENT PILLAG DATE: 1905-00-10 PRIOR APPLICATION NUMBER: US 09/382,242 PRIOR FILING DATE: 1995-00-16 PRIOR FILING DATE: 1995-00-16 PRIOR PILLAGION NUMBER: US 08/602,359 P	RESULT 3 US-09-903-410-26 Sequence 26, Application US/09903410 Patent No. US20020146799A1 GENERAL INFORMATION: APPLICANT: DIVERSA CORPORATION APPLICANT: MURPHY, Demnis APPLICANT: MURPHY, Demnis APPLICANT: RSID, John APPLICANT: MAFFIA, Anthony APPLICANT: SWANSON, Ronald APPLICANT: SWANSON, Ronald APPLICANT: SWANSON, Ronald APPLICANT: WARREN, Patrick	Db 361 AGGGCTCTATACCTCTCGAAAGGGAATTACCTCGCACTTCTCGGCAGCTGTGCAATT 420 421 CCCGGCATATTTGAACCCGTTGAGTATAAGAATTACTTGCTCGTTGACGAGCTATAGTT 480 421 CCCGGCATATTTGAACCCGTTGAGTATAAGAATTACTTGCTCGTTGACGAGGTATAGTT 480 421 CCCGGCATATTTGAACCCGTTGAGTATAAGAATTACTTGCTCCGTTGACGAGGTATAGTT 480 481 AACAACCTTCCCGTTGAGCCCTTTCAGGAAAGCGGTATTCCCACCCGTTGAGGAGTATAATT 480 481 AACAACCTTCCCGTTGAGCCCTTTCAGGAAAGCGGTATTCCCACCCGTTTGAGGAGCTTC 540 481 AACAACCTTCCCGTTGAGCCCGTTTCAGGAAAGCGGTATTCCCACCCGTTTGAGGAGCTTC 540 481 AACAACCTTCCCGTTGAGGCCCGTAAAAGAACATTCTTCACATCCTTTTGAGGAGCTTC 600 541 CTTCCCATAGAGCCGGAAAAGGATATAAAGAACATTCTTCACATCCTTTTGAGGAGCTTC 600 541 CTTCCCATAGAGCCGGAAAAGGAATAAAGAACATTCTTCACATCCTTTTGAGGAGCTTC 600 601 TTTCTTGCGGTCCGCTCAAACTCCCGAAAAGAGAAAGAGTTTTTGTGACCTCGTTATAGTT 660 601 TTTCTTGCGGTCCGCTCAAACTCCCGAAAAGAGAAAGAGTTTTTTTT
RESULT 4 US-10-027-805-29 Sequence 29, Application US/10027805 Patent No. US20020164725A1 GENERAL INFORMATION: REID, John MAFFIA, Anthony LINK, Steven SWANSON, Ronald V. WARREN, Patrick V. KOSMOTKA, Anna TITLE OF INVENTION: ESTERASES NUMBER OF SEQUENCES: 42 CORRESPONDENCE ADDRESS: ADDRESSEE: FISH & RICHARDSON P.C. STREET: 4225 EXECUTIVE SQUARE, STE 1400 CITY: LA JOLLA STATE: CALIFORNIA COUNTRY: USA ZIP: 92037 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER: IMP BS/2 OPERATING SYSTEM: MS-DOS SOFTMARE: WORD PERFECT 6.0 CURRENT APPLICATION NUMBER: US/10/027,805 FILING DATE: 21-Dec-2001 CLASSIFICATION: <unknown></unknown>	OY 601 TITCTTGCGGTCCGCTCAAACTCCTCGAAAAGAACATTCTTCTGAGGAGCTTC 600 QY 601 TITCTTGCGGTCCGCTCAAACTCCGAAAAAGAACATTCTTTGTGACCTCGTTATAGTT 660 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	181 GGGATGTTCAGCCTTCTGAAGAGGTTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCT

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                     Length 750;
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                                                                       NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REPERENCE/POCKET NUMBER: 09010/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPRAX: 619-678-5099
                                                                                                                                                                                                                                                                                TOPOLOGY: LINEAR

MOLECULE TYPE: GENOMIC DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-027-805-29
: APPLICATION DATA: APPLICATION NUMBER: 08/602,359
                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 750 MCLEOTIDES
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                   FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 29
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: ILM PS/2
COMPUTER: MAS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/10/027,804
FILING DATE: 21-Dec-2001
CLASSIFTCATION DATA:
APPLICATION DATA:
RILING DATE: CURRINGMA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                          ADDRESSEE: FISH & RICHARDSON P.C. STREET: 4225 EXECUTIVE SQUARE, STE
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MOLECULE TYPE: GENOMIC DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
Sequence 29, Application US/10027804
Publication No. US20030054530A1
GENERAL INFORMATION:
REID, John
MAFFTA, Anthony
LINK, Steven
SWANSON, Ronald V.
WARREN, Patrick V.
KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 091
TELECOMMUNICATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                      CITY: LA JOLLA
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; ORGANISM: Aquifex VF5-34LC
US-09-903-410-29
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                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ENZYMES HAVING ESTERASE ACTIVITY AND METHODS OF USE THEREOF FILE REFERENCE: DIVERILAGO.

CURRENT APPLICATION UNMERR: US/09/903,410

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 09/382,242

PRIOR FILING DATE: 1999-08-24

PRIOR PILING DATE: 1996-08-24

PRIOR PILING DATE: 1996-08-24

PRIOR PILING DATE: 1996-08-24

PRIOR FILING DATE: 1996-08-24

PRIOR FILING DATE: 1996-08-24

PRIOR FILING DATE: 1996-03-16

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin version 3.0

LEQ ID NO 29

LENGTH: 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Application US/09903410 Patent No. US20020146799A1
                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 516; Conserv
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APPLICANT:
APPLICANT:
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APPLICANT: MAFFIA, Anthony
APPLICANT: LINK, Steven
                                                                                                                                                                                                                                                                                                                               ENGTH: 750
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                                                 ATAGCCCACATAGGTGTTTTGAAAGCTATAAACGAGCTCGGTATAAAGGGTGAGGGCTTTA 120
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                          ATCGCCCATATAGGTGTTTTAAAAGCTCTGGAAGAGCTCGGTATAAAGGTAAAGAGGCTC
                                                                                                                                  TTGAGATTGAGGAAATTTGAAGAGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGC
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REID, John
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                                                                                                                                                                                      Conservative
                                                                                                                                                                                                     52.6%;
                                                                                                                                                                                    Score 397.8; DB 10; Length Pred. No. 4e-125; o; Mismatches 197; Indels
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                                                                                                                                                                                               APPLICANT: Lassner, Michael
APPLICANT: Metz, James G
APPLICANT: Metz, James G
APPLICANT: Metz, James G
APPLICANT: Metz, James G
TITLE OF INVENTION: SCHIZOCHYTRIUM PKS GENES
FILE REFRENCE: CONE.131.02US
CURRENT PILLING DATE: 2002-12-27
PRIOR PILLING DATE: 2002-12-27
PRIOR APPLICATION NUMBER: US/09/231,899
PRIOR FILLING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/048,650
PRIOR FILING DATE: 1999-06-04
PRIOR FILING DATE: 1997-06-04
PRIOR FILING DATE: 1998-06-04
NUMBER: OF SEQ ID NOS: 86
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 40138
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US-10-331-061-12
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                                                                                                                                               US-10-331-061-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/10331061 Publication No. US20030101486A1 GENERAL INFORMATION:
                                                                 Matches
                                                                                Query Match
Best Local (
                                                                                                                                                              ORGANISM: Vibrio marinus
                                                                                                                                                                                    TYPE: DNA
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23 AGATAAACCTCGTTCTTTCGGGAGGGGCTGCAAAGGGGCATAGGCCCACATAGGTGTTTTGA 82
                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTGAGCTTGAGGAGTTCACACCCCCTTGATGTTAGAAAAGCGGACCAAATAAT 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTCTTGCGGTCCGCTCAAACTCCGAAAAGAGAAAAGGAGTTTTGTGACCTCGTTATAGTT 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCCCATAGAGCCGGAAAAGGATATAAAGAACATTCTTCACATCCTTTTGAGGAGCTTC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACAACCTTCCCGTTGAGCCCTTTCAGGAAAGCGGTATTCCCCACCGTTTGCGTTGATGTC 540
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                                                                 Conservative
                                                                                6.1%;
                                                            Score 46.2; DB 9;
Pred. No. 0.00046;
0; Mismatches 88;
                                                                 88;
                                                                                                 Length 40138;
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Sequence 1639, Application US/09938842A

Sequence 1639, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

TITLE OF INVENTION: SAME, AND METHODS OF USB

TITLE OF INVENTION: SAME, AND METHODS OF USB

TITLE OF INVENTION: SAME, AND METHODS OF USB

TITLE OF INVENTION: SAME, AND METHODS OF USB

TITLE OF INVENTION: SAME, AND METHODS OF USB

TITLE OF INVENTION: SAME, AND METHODS OF USB

TITLE OF INVENTION: SAME, AND METHODS OF USB

TITLE OF INVENTION UNMERR: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/201,61

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-08-24

WUMBER: OF SEQ ID NOS: 5379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGCGCTTGAAAACGGGGCTTCCGATTTAAAAGGCTGGCCGGAACGAGCGCCGGTTCGA 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 GGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTGATAGGGTGGG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 AATTAAATGAAAGCGAGCTCCTTGACCCGAGGTTTTCACTCTTGCCTTTGAAATTGCTGC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 Acaircacogogiririricaescescereaaaasescrirecerreresaascarace 64
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                                                                                            GENERAL INFORMATION:

APPLICANT: Berka, Randy M.

APPLICANT: Clausen, ID Groth

TITLE OF INVENTION: Methods For Monitoring Multiple Gene

TITLE OF INVENTION: Expression

FILE REFERENCE: 10085.500-US

CURRENT APPLICATION NUMBER: US/09/974,300

CURRENT APPLICATION NUMBER: 09/680,598

PRIOR PILING DATE: 2000-10-06

PRIOR FILING DATE: 2001-10-06

PRIOR FILING DATE: 2001-03-27

NUMBER: FASTSEQ for Windows Version 4.0

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 876
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Pred. No. 0.18;
0; Mismatches 132;
                     Sequence 2350, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2350
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 46.6%;
Matches 115; Conservative (
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LENGTH: 1062
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14817 AAATTGSCTTAGTCCTTTCTGGCGGTGGTGCTAAAGGTATTGCTCATCTTGGTGTATTAA 14876
                                                                                                                         14877 AATACCTGTTAGAGCAAGATATAAGACCGAATGTAATTGCGGGTACAAGTGCTGGCTCTA 14936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 GAAGGCTATAAGATTCCTTGAGGAAGTTCTCCCTTACAGGAGAATAGAAAACTTGAGAT 323
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                                                                                                                                                                                             143 TCGTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAAGGGATGTTCAGCCTTCTGAAGA 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 dairggacriedectriegereregegegeragagerriegeceacarriegrereraaa
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                                                                83 AAGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTAAGCGGGGTGAGCGCCCGGGGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10065.500-01
FURRENT APPLICATION NUMBER: 09/680,598
PRIOR PLILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR PLILING DATE: 2000-10-3-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 6748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45.8; DB 10; Length Pred. No. 4.7e-05; o. Mismatches 232; Indels
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Patent No. US20020146721A1
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Best Local Similarity 44.4%;
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA; ORGANISM: Bacillus clausii
US-09-974-300-6748
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NAME/KEY: CDS
LOCATION: (35)..(1093)
COTHER IMPORMATION: G1022
US-10-295-403-89
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PLANT GENE SEQUENCES I
FILE REFERENCE: MBI-0003
CURRENT APPLICATION NUMBER: US/10/295,403
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US/09/394,519
PRIOR FILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR RICING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/101,349
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/103,312
PRIOR APPLICATION NUMBER: 60/103,312
PRIOR APPLICATION NUMBER: 60/108,734
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/108,734
PRIOR FILING DATE: 1998-11-17
PRIOR PILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 170
PRIOR PILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 170
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US-10-295-403-89
Sequence 89, Application US/10295403
Publication No. US20030101481A1
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                                                                                                                                                                                                                                                                                                   SOFTWARE: Pater
SBQ ID NO 89
LENGTH: 1390
                                                                             Query Match 4.6%; Score 35; DB 9; Length 1390 Best Local Similarity 49.2%; Pred. No. 0.43; Matches 92; Conservative 0; Mismatches 95; Indels
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Best Local Similarity
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                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Arabidopsis thaliana
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                           196 CTGAAGAGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTGATA 255
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Jiang, Cai-Zhong
Keddie, James
Zhang, James
Benito, Maria-Ines
Yu, Guo-Liang
Yu, Guo-Liang
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CCGCGGCGCGAAAATGGAAGATACCGCTTTGAGAGAAGCTGCTTCTGCAGGGATTCACG 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Broun, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adam,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riechmann, Jose Luis
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US-10-184-644-546
US-10-184-644, Application US/10184644
Sequence 546, Application US/10184644
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US-10-184-644-546
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LENGTH: 458
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapp
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zhang, Zemin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                  278 TCCTTGAGGAAGTTCTCCCTTACAGGAGAATAGAAAACTTGAGATACCGACGTATATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 AVLKGLYLLRSKPDRAQHAATKCTSPSTELSITSRGATLLVAKTKASPAGKLEARAALNQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   458
TTCACATCCTTTTGAGGAGCTTCTTTCTTGCGGTCCGCTCAAACT 6:22
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                                                                                                                                CACTTCTCGGCAGCTGTGCAATTCCCGGCATATTTGAACCCGTTGAGTATAAGAATTACT 457
                                                                                                                                                                                                                                                                                              HEKALVNRDRTLPLVEEIDQRYFSIIDSKVKKVMSIPKGNSALRRVMEETYYHHIYHTVA
                                                                                                                                                                                                                                                                                                                                     GCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCGGAAGGGAGTTTAATCCCCCG
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                                                         ALAHYKLVYIHPFIDGNGRTSRLLMNLILMQAGYPPITIRKEQRSDYYHVLEAANEGDVR 412
                                                                                              TTCCCACCGTTTGCGTTGATGTCCTTCCCATAGAGCCCGGAAAAGGATATAAAGAACATTC
                                                                                                                                                                                                                   IEGNTLTLSEIRHILETRYAVPGKSLEEQNEVIGMHAAMKYINTTLVSRIGSVTISDVLE
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                                                                                                                                                                             TGCTCGTTGACGGAGGTATAGTTAACAACCTTTCCCGTTGAGCCCTTTCAGGAAAGCGGTA 517
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Pan Janna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pan, James
Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard, Audrey
Godowski, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.4%; Score 33.2; DB 9; ilarity 9.9%; Pred. No. 0.94; Conservative 113; Mismatches 252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLYPEPTIDES AND NUCLEIC
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APPLICANT: Han, B.
APPLICANT: Han, B.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REFERENCE: 1360.001US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 5520;
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                                                                                                                                                                                                                                                                SOFTWARE: FRACESO for Windows Version 2.0b CURRENT APPLICATION DATA:
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.4%; Score 33.2; DB 9;
50.0%; Pred. No. 4;
tive 0; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/015W01
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION UNMER: US/09/202,681A
RFILING DATE: 23-Dec-1999
APPLICATION NUMBER: 08/666,857
FILING DATE: 19-JUN-1996
APPLICATION NUMBER: 60/033,752
FILING DATE: 19-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/902,525
FILING DATE: 09-Jul-2001
CLASSIFICATION: <Unknown>
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MOLECULE TYPE: Genomic DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-902-525-38
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                                                                                                                                                                                                                                                     OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
                                                                                                                                                                                                                             COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 66, Application US/09887576 Patent No. US20020144047A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           COMPUTER READABLE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83; Conservative
                                                                                                                         COUNTRY: USA
ZIP: 92037
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GENERAL INPORMATION:
APPLICANT: Budworth, P.
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Matches 83; Congert
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Chang, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  338 GCGCCACKGATTTATACTCCGGAAGGGCTCTATACCTCTCGGAAGGGAGTTTAATCCCCG 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME PLEE REFERENCE: P3430R1C217 CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT APPLICATION NUMBER: 2002-06-29
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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413 PFIRFIAKCTETTLDTLLFATTEYSVALPEAQPNHSGFKETLPVK 457
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4.4%; Score 33.2; DB 9; Length 4.
Best Local Similarity 9.9%; Pred. No. 0.94;
Matches 40; Conservative 113; Mismatches 252; Indels
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TITLE OF INVENTION: THERMOSTABLE PHOSPHATASES
NUMBER OF SEQUENCES: 54
                                                                                                                      Sequence 546, Application US/10184634
Publication No. US20030068684A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 38, Application US/09902525
Patent No. US20020164751A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe, Colin K. Wood, William I.
                                                                                                                                                                                                                                                Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                    Pan, James
Smith, Victoria
                                                                                                                                                                                                APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-634-546
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                                                                                                 US-10-184-634-546
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LENGTH: 458
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CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-12-29
NUMBER: OP SEQ ID NOS: 875
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66
LENGTH: 2000
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-887-576-66
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  밁
                                                                                                                                                                                                                                                                                                                              Query Match 4.3*; Score 32.8; DB 10; Length 2000; Best Local Similarity 52.1*; Pred. No. 3; Matches 73; Conservative 0; Mismatches 67; Indels 0; Gaps
308 TTTTACATTCAGGCTCTTAC 327
                                   155 TTTATGCCTCAGGCTACTCC 174
                                                                                                                                                                                                                      188 TITTITTGTATATGCAGCCATGCACAAAAGCCCCCAACGGTACGTTGAAACATATATGAT 247
                                                                                                           248 ATCAMAMATAATGTTGATGGATTTGATCATAGTTGGACAAGTGTTTTACGTATATATTT 307
                                                                                                                                              95 AGCTCGGTATAAGGGCTGAGGGCTTTAAGCGGGGTGAGCGCCGGGGCAATCGTTTCGGTCT 154
                                                                                                                                                                                                                                                                        35 TTCTTTCGGGAGGAGCTGCAAAGGGCATAGGCCACATAGGTGTTTTGAAAGCTATAAACG 94
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Search completed: June 19, 2003, 15:01:24 Job time : 123 secs

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Title:
Perfect score:
Sequence:
                                                                              Regult
No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
     00000
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                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                               Score
    47.2
41.8
40.8
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Match
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Gapop 10.0 , Gapext 1.0
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756
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(without alignments)
11368.420 Million cell updates/sec
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     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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  BF657575
BM107729
AV397710
BI875128
BQ816618
BQ816618
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BF657575 OV2_23_H0
BM107729 c01603 cD
AV397710 AV397710
B1875128 963122A09
BQ816618 1030058H1
BQ817181 1030062C1
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180 MARC	AW29	10	298	4.4		44
AL420700 T3 end of		17	979		Ψ	3
AQ279281 CITBI-E1-	AQ27	17	356		Ü	42
AL076805 Drosophil	CNS	17	898		Ψ	11
AG103741 Pan trogl	AG10	17	812		ω	0
AG077885 Pan trogl	AG07	17	668		·	99
Pog.		17	619		w	8
AZ010196 RPCI-23-3		17	596		Ü	37
	BQ143278	14	426	4.5	33.8	8
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BE935559 MR2-MT012		12	385		ω	4
057P53U		9	408		34	ພ
BH760289 BMBAC312A		17	361	٠	34	32
AG154803 Pan trogl		17	633	4.5	4.	31
AQ672914 HS 5460 A		17	542			ö
2342		10	461			29
3161		17	668	4.6	4.	8
9057		؈	816			27
BQ796737 EST 5675		14	789	4.6	4.	26
9514		14	589		4	25
5890		17	463		34.8	24
BQ797080 EST 6018		14	449			23
BM479230 AGENCOURT		13	1101	4.6	35	22
AI992658 701558595		ø	569		35	21
AV831633 AV831633		10	528		35	80
R30038 12643 Lambd		14	508	4.6	35	61
BG845295 1024009F1		12	767		5	8
AL065414 Drosophil		17	1101		Ġ	17
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HS 5318	AQ60081	17	510		ω.	Ξ
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	AZ51786	17	460	•	40.2	7

ALIGNMENTS

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FEATURES									COMMENT	JOURNAL	TITLE		AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BF657575
Location/Qualifiers	POLYA=No.	High quality sequence stop: 392	Email: mmpratt@uga.edu	Fax: 706 583 0210	Tel: 706 542 1860	Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA	The University of Georgia, Department of Plant Biology	Laboratory for Genomics and Bioinformatics	Contact: Cordonnier-Pratt MM	Unpublished (2000)	An EST database from Sorghum: ovaries of varying immature stages	, L.H.	Cordonnier-Pratt, MM., Gingle, A., Marsala, C., Sudman, M. and Pratt	1 (bases 1 to 392)	<pre>clade; Panicoideae; Andropogoneae; Sorghum.</pre>	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC	<pre>Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;</pre>	Sorghum bicolor	sorghum.	EST.	BF657575.1 GI:11922709	BF657575	sequence.) Sorghum bicolor cDI	BF657575 392 bp mRNA linear EST 20-DEC-2000	

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456 bp mRNA linear EST 23-APR-2002 AV397710 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii AV397710 AV397710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                   537 IGTCCTTCCCATAGAGCCGGAAAAGGATATAAAGAACATTCTTCACATCCTTTTGAGGAG 596
                                                                                                                                                                335 TTAAATTATCAAGGCGACCAAATGTGTNTGGAAGAGCATGAATCTGATTATTGCTGAGAT 276
                                                                                                                                                                                                                            CITCITICITGCGGTCCGCTCAAACTCCGAAAAGAAAGAAAGGAGTTTTGTGACCTCGTTAT 656
                                                                                                                                                                                                                                                      275 CCAATTCCCTGAGGTTAGCCAAATCACCAAATGTWTCAGGAAGTTCTTTGAGGTCACTGA 216
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Bukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

Chlamydomonadaceae; Chlamydomonas.

(bases 1 to 456)

Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa; H. and Tabata,S.

A large scale structural analysis of cDNAs in a unicellular green alga, Chlamydomonas reinhardtii. I. Generation of 3433

non-redundant expressed sequence tags

DNA Res. 6 (6), 369-373 (1999)
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/db xref="taxon:3055"
/db xref="c149b11r"
/clone="C149b11r"
/clone lib="Chilamydomonas reinhardtii C9"
/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                             477 AGTTAACAACCTTCCCGTTGAGCCCTTTCAGGAAAGCGGTATTCCCCACCGTTTGCGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460 CTCGTTGACGGAGGTATAGTTAACAACCTTCCCGTTGAGCCCTTTCAGGAAAGCGGTATT
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    Indels
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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Pred. No. 0.29;
0; Mismatches
    Mismatches
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                                                                                                                                                                                                                                                                                                                657 AGTICCTGAGCTTGAGGAG
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1 Similarity 59.5%;
69; Conservative
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    Conservative
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Best Local Similarity
Matches 69; Conserv
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LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AV397710/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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AUTHORS
TITLE
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                                      /db_xref="taxon:4558"

/db_xref="taxon:4558"

/clone lib="Ovary 2 (0V2)"

/note="Organ: Mix of ovaries of varying immature stages
from 8-week-old plants; Vector: pBluescript II from Lambda
Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made
from poly-A RNA in the cloning vector lambda ZAP II.

from poly-A RNA in the cloning vector lambda EAP II.

94 c 104 g 115 t
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
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/tissue_type="Cotyledons"
/dev_stage="Eight days post germination"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from soybean cv. Century cotyledons 8 days g
                                                                                                                                                                                                                                                                                                                Gaps
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Matthews, B.F., Khan, R., MacDonald, M. and Beard, H.
Resistance mechanisms in soybean: Gene expression profile at
early stage of soybean cyst nematode invasion
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                Query Match
6.2%; Score 47.2; DB 12; Length 392;
Best Local Similarity 56.4%; Pred. No. 0.0028;
Matches 88; Conservative 0; Mismatches 68; Indels 0
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Pred. No. 0.14;
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                     organism="Sorghum bicolor"
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Fax: 301 504 5728
Email: alkharon@ba ars.usda.gov.
Location/Qualifiers
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/db_xref="taxon:3847"
/clone="c01e03"
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                                                                                        BQ816618.1 GI:22065882
BQ816618.1 GI:22065882
EST.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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1 (bases 1 to 657)

Grossman, A., Chang, C.-W., Davies, J., Harris, B., Hauser, C., Lef
Grossman, A., Chang, C.-W., Silflow, C. and Stern, D.
,P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation
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BI875128.1 GI:16073132
                                                                                                                                                                                                                                                                                       BQ816618
1030058H11.yl C. reinhardtii CC-1690, Deflagellation (normal Lambda Zap II Chlamydomonas reinhardtii CDNA, mRNA sequence.
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Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
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Durham, NC 2770
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                                                                                     Chlamydomonadaceae; Chlamydomonas
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/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress condition I,
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Pred. No. 0.36;
0; Mismatches 47;
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Matches 69
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Location/Qualifiers
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TITLE
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Grossman, A., Chang, C.-W., Davies, J., Harris, B., Hauser, C., Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1030
Unpublished (2002)
Contact: Charles Hauser
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Unpublished (2002)
Contact: Charles Hauser
                                                                                                                                                                                                                                                                                                                                                                                                                          BST.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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Tel: 919 613 8159
Fax: 919 613 8177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQ817181 Tinear EST 01-A BQ817181 Linear EST 01-A BQ817181 C. reinhardtii CC-1690, Deflagellation (normal Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Duke University
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                                                                                                                 DCMB Box 91000
Duke University
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                                                                                          Durham, NC 27708-1000
                          Tel: 919 613 8159
Fax: 919 613 8177
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/strain="CC-1690 wild type mt+ 21gr"
/db xref="taxon:3055"
/db xref="taxon:3055"
/clone lib="C. reinhardtii CC-1690, Deflagellation
(normalized), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
xhoI; Deflagellation library, constructed by John Davies
and Jeffrey McDermott, combines cDNAs from CC-1690 cells
which had been re-synthesizing flagella for 15, 30 and 60
min after being deflagellated by pH shock. PolyA mkNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda Zap II
(Stratagene) in the EcoRI (5') and XhoRI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with Exassist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al., (1996) Genome Research 6: 791-806."
chauser@duke.edu
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Pred. No. 0.36;
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614

source

BASE COUNT ORIGIN

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BG784079 807 bp mRNA linear EST 20-MAY-2001
SEAUMC004036 Sea urchin primary mesenchyme cell cDNA library
Strongylocentrotus purpuratus cDNA clone PC_0020_A1_B12_MR 5', mRNA
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Zhu, X., Mahairas, G., Illies, M.R., Cameron, R.A., Davidson, E.H. and
Ettensohn, C.A.
                                 /clone="RPCI-11-89H18"
/clone_lbb="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3-6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
79     95     9     140 t
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Development 128 (13), 2615-2627 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         555 GGAAAAGGATATAAAGAACATTCTTCACATCCTTTTGAGGAGCTTCTTTGCGGTCCG
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Corganism="Strongylocentrotus purpuratus"
db xref="taxon:7668"
/clone="PC_0020_A1_B12_MR"
/clone="PC_0020_A1_B12_MR"
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Eucchinoldea; Echinocea; Echinoida;
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Pred. No. 0.71;
0; Mismatches 45; Indels
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.rhes 45; Indels
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/lab_host="B.coli"
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Carnegle Mellon University
4400 Fifth Avenue, Pittsburgh, PA 15213, USA
Tel: +1 412 268 5849
Email: ettensohn@andrew.cmu.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                                                                                                           DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strongylocentrotidae; Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                   Score 40.2; DB Pred. No. 0.44; 0; Mismatches
/db xref="taxon:9606"
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ilarity 56.4%;
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Dept. Biol. Sci.
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    /organism="chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_rare="texon:3055"
/clone lib="C. reinhardtii CC-1690, Deflagellation
|/clone lib="C. reinhardtii CC-1690, Deflagellation
| normalized), Lambda Zap II"
|/note="Vector: pBluescript II SK-; Site I: BCORI; Site 2:
|/note="Vector: pBluescript II SK-; Site I: BCORI; Site 2:
|/note="Vector: pBluescript II SK-; Site I: BCORI; Site 2:
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|/note="Vector: pBluescript II SK-; Site I: BCORI; Site 2:
|/note="Vector: pBluescript II SK-; Site II SK-; 30 and 60
|/note all addition of the sample, pooled and cDNA synthesized.
|/note="Vector: pBluescript II SK-; plasmids were excised from the lambda |
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Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (info@resegen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac.end_search/bac_end_search.html.

This BAC end was generated during the R&D process and may have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 460)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
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Other GSSs: RPCII1-89H18.TJ RPCII1-89H18.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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ob_xref="GDB:7533977"
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Class: BAC ends.
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VERSION KEYWORDS SOURCE ORGANISM

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Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: T7
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Plate: 583 row: O column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 Queen Anne Avenue North, Seattle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center University of Washington
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AQ332328
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Proc. Natl. Acad. Sci. U.S.A. 96 (17),
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Keller,A., Shaker,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 459)
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                                                                                                                          GAAGGGAGTTTAATCCCCGCACT 401
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          GTATGCAAATATATCTCCTCAGT
                                                                  GAGCTGAAAACACATAGAAGCTGTACTCATTTCTATTCACAAAGAACTGTTCTACTGTCT
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Location/Qualifiers
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(206) 616-3887
                                                                                                                                                                                                                                                                                                                                        /cell_type="Lymphocytes"
/note="Vector: pBACe3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                   /clone="Plate=583 Col=14
/clone_lib="RPCI11 Human
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Pred. No. 0.58
0; Mismatches
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74 g 159 t 1 others .
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AQ335962/c
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AQ600815 510 bp DNA linear GSS 10-JUN HS_5318_A2_C09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=894 Col=18 Row=E, DNA sequence.
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Query Match
Best Local Similarity
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Seq primer: SP6
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Clones may be purchased from Research Genetics (info@resgen.com)
BAC end Web Server: http://www.htsc.washington.edu
Plate: 591 row: J column: 13
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 465)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. ar
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                                             GAAGGGAGTTTAATCCCCGCACT 401
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                                                                                                                                  GAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCG 378
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  GTCTGCÁAATAAATCTCCTCÁGT
                                                                                        GAGCTGAAAACACATAGAAGCTGTACTCATTTCTATTCACAAAGAACTGTTCTACTGTCT
                                                                                                                                                                                149
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; RPCI11 Human Male
76 C 76 G 162 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="Plate=591 Col=13"
clone_lib="RPCI11 Human"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sex="Male"
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db_xref="taxon:9606"
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49.8%;
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                                                                                                                                                                                                                                                                                                                                                                  Score 39.8; DB 17;
Pred. No. 0.59;
0; Mismatches 102;
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GSS 10-JUN-1999

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GSSBru0818 Sheared genomic library Brucella melitensis biovar Abortus genomic clone B23, DNA sequence.
                                                                                                                                                                                                                               Direct Submission

Submitted (23-UUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EWR cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre Tribrary (Dros DAC) was prepared from embryos by Alain Bucheton project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 AGGAGCTGCAAAGGGCATAGCCCACATAGGTGTTTTGAAAGCTATAAACGAGCTCGGTAT 104
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Drosophila melanogaster.
Drosophila melanogaster.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bhydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1010)
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Organism="Drosophila melanogaster"
(db xref="taxon:7227"
(clone="BACN16C05"
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/plasmid="pBeloBAC11"
/note="end : SP6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: jwallacedu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones availability, please conteact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
plate: 894 row: E column: 18
                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                         Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
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                                                                                                                                                                                                                                                                                                                                                                             Sequence-tagged connectors: A sequence approach to mapping and
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                                                                                                                                                                                                                                                                                                                                                                                               scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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/clone="Plate=894 Col=18 Row=E"
/clone lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
Vol Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
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organism="Homo sapiens"
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Cliften, P.F., Hillier, L.W., Fulton, L., Graves, T., ,W.R., Waterston, R.H. and Johnston, M. Surveying Saccharomyces genomes to identify functions.
                                                                            Saccharomyces mikatae

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                            AZ924693

462 bp DNA linear GSS 01-Al 4906.id55b14.sl Saccharomyces mikatae IFO 1815 Saccharomyces mikatae genomic clone 4906.id55b14.sl, DNA sequence.
                                                                                                                                                          GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sanchez, D.O., Zandomeni, R.O., Cravero, S., Verdun, R.E., Pierrou, E., Faccio, P., Diaz, G., Lanzavecchia, S., Aguero, F., Frasch, A.C.C., Andersson, S.G.E., Rosetti, O.L., Grau, O. and Ugalde, R.A. Gene discovery through genomic sequencing of Brucella abortus Infect. Immun. 69 (2), 865-868 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ049266.1
GSS.
                                                                                                                                    Saccharomyces mikatae.
                                                                                                                                                                            AZ924693.1 GI:13495592
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Instituto Nacional de Tecnologia Agropecuaria (INTA) C.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Zandomeni, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brucella melitensis biovar Abortus.
Brucella melitensis biovar Abortus
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                                                                                                                                                                                                                                                                                                                                                                                       TTCCCGTTGAGCCCTTTCAGGAAAGCGGTATTCCCACCGTTTGCGTTGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTTGCGCCGGTGCGCCGATGGCCGCATTCTGGTCGATGGCGGGCTGTTCAATCCGG
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                                                                                                                                                                                                                                                                                                                                                   TGCCGTTCGACCTCCTTTTCGACAAGGCGGATATCGTCATCGGCATCGATGT
                                                              (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elar. Buenos Aires,
5411-4621-3316/1683
5411-4481-1316
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ilarity 47.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        size-fractionated by agarose gel electrophoresis.
Fragments between 1.5-3 Kb were recovered and ligated
the EcoRV site of the pBluescript SK (-) vector."
112 c 97 g 63 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Brucella melitensis biovar Abortus"
|strain="S-2308"
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  identify functional
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Washington University Medic
Box 8232, 4566 Scott Ave.,
Tel: 314 362 2735
Fax: 314 362 7855
                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, I
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1244)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF678161 1244 bp mRNA linear EST 21-DEC-2 602084827F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248967 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comparative DNA sequence Unpublished (2001)
                                                                                                                         Plate: LLCM1068 row: f column:
High quality sequence start: 6
High quality sequence stop: 88.
                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF678161.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mj@genetics.wustl.edu
Class: random plasmid subclone.
                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Johnston M
                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGAAATTTGAAGAGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCATAGCCCAC
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/clone="IMAGE:4248967"
/clone_lib="NIH_MGC_83
/lab_host="DH10B (T1 pl
                                                                                                        Location/Qualifiers
                                                   organism="Homo sapiens
db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Saccharomyces mikatae
/note="Random genomic sequence "
107 c 72 g 141 t
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/strain="IPO 1815"
/db_xref="taxoon:114255"
/clone="4906.id55b14.51"
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Catarrhini; Hominidae;
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phage-resistant)"

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Site 1: Sfil (ggcgctctcggcc); Site 2: Sfil (ggccattatggcc); 5, and 3, adaptors were used in cloning as follows: 5, and 3, adaptors were used in cloning as follows: 5, adaptor sequence: 5, -CACGCCATATGGCCA, and 3, adaptor sequence: 5, -CACGCAATATGGCCA, and 13, adaptor sequence: 5, -CACGAAGCCGAAGCGGCGACATC-dT(30)BN-3, (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412 TGTGCAATTCCCGGCATATTTGAACCCGTTGAGTATAAGAATTACTTGCTCGTTGACGGA 471
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         pDNR-LIB (Clontech);
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Search completed: June 19, 2003, 14:21:01 Job time : 1081 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Database
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Pred. No. 18 the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. 000 a 0.0 a Ω a 403.6 63.8 57.2 55.4 55.2 447.48 450.000.48 53.6 53.6 Score Match Query 6.1 998 6.1 467 5.8 218470 5.8 282700 5.8 349619 5.7 11010 5.7 211018 5.6 10593 5.4 10029 5.3 253945 5.3 310001 5.3 310001 5.2 269223 5.2 269223 6.9 9831 6.9 172325 6.9 300950 6.6 10410 6.6 291136 7.6 11039 7.3 11618 7.3 2797 7.3 329100 7.1 903 7.1 340806 5.9 903 2266 22388 22388 254050 1 40138 1 41587 15820 11357 11039 Length 3653 10648 13860 16397 23203 DB BCH410309 A96530 SFTYRT AE008778 AL627269 AR1162864 AB025342 HSA325659 AX438333 BSUB0013 BACUH642 AE0090301 CNS07EGC A96524 AE003860 AE009531 AB004756 AB013136 BCU224437 BCU224437 SME591787 A96528 NMA1Z2491 A96526 AB002562 AX044035 AP001516 AB0025560 AP0025560 ACCOTGSA AE000221 D90759 AF404759 AX067466 AF026065 AE000737 AE012939 Ħ D90852 AF178030 SUMMARIES A96530 Sequence 56 X66849 S.flexneri AB008778 Salmonell AL627269 Salmonell AR118084 Sequence AB025342 MORITElla AJ325659 Homo sapi AX43833 Sequence Z99116 Baccillus su D84432 Baccillus su D84432 Baccillus su AB002996 Mesorhizo AE008096 Agrobacte AL5090445 chromosom AF404759 Bacteroid AX067466 Sequence AF026065 Ralstonia B22111 Aromatic co 166494 Sequence 14 AC105161 Mus muscu AC023142 Homo sapi AF178030 Homo sapi D90758 Escherichia D90759 Escherichia D90852 E.coli geno AJ410309 Erwinia c A96526 Sequence 55 AE002562 Neisseria AX044035 Sequence AP001516 Bacillus AE005340 Escherich AB004756 Pseudomon AB013136 Thermoana AJ224437 Brwinia c AL591787 Sinorhizo A96524 Sequence 55 AE003860 Xylella f AE009531 Brucella AP002556 Escherich M64675 Escherichia AE000221 Escherich A96528 Sequence 56 AL162752 Neisseria AE000737 Aquifex a AE012939 Chlorobiu Description

ALIGNMENTS

TITLE	AUTHORS	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AE000737	RESULT 1
Graham,D.B., Overbeek,R., Snead,M.A., Keller,M., Aujay,M., Huber,R., Feldman,R.A., Short,J.M., Olsen,G.J. and Swanson,R.v. The complete genome of the hyperthermophilic bacterium Aquifex	Deckert, G., Warren, P.V., Gaasterland, T., Young, W.G., Lenox, A.L.,	Bacteria; Aquificae; Aquificae; Aquificales; Aquificaceae; Aquifex. 1 (bases 1 to 15820)	Aquifex aeolicus	Aquifex aeolicus.	•	AE000737.1 GI:2983782	AE000737 AE000657	Aquifex aeolicus section 69 of 109 of the complete genome.	AE000737 15820 bp DNA linear BCT 25-MAR-1998		

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LKNMIKGMTLVLSDLRVKEQNMRKASGNFLLITDIANYLVEKGVPFRTAHHIAGSIVA
YLLEKGKKLBEMTLEEFKQPSEKPEEDVFDILSPERAADRKRVYGGTAKEEILRIIEV
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product="NADH dehydrogenase I chain H"
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db_xref="GI:2983790"
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db_xref="GI:2983791"
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|db_xref="G1:2983789"
                                                                                                                                                                                                                                                       /note="aq_1372"
3099. .4472
/gene="argH"
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4548. .5327
/gene="nuoH2"
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/gene="nuoH3"
/note="aq 1374"
5294. .5596
/gene="nuoH3"
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/gene="nuo12"
/note="aq 1375"
5603. .6229
/gene="nuo12"
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/transl_table=11
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226. .6762
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'transl_table=
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trans table=
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/gene="nuoH2"
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'gene="nuoJ2"
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/gene="argH"
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                                                                                                                                                                                                                                                                                                      Submitted (12-JUL-1997) Diversa Corporation, Genomics, San Diego, CA 92121
Putative indicates no similarity to known proteins
Hypothetical indicates similarity to a protein of unknown function.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDTGFFVLDESIFEVAEEALKEQKKLTMSELAKRAQIPCTEVSGYFWNDVDTPEDVEK
AKKYLVKTAIKGVGDGFISRNLARKVSTRISPYLVDKFTPNQLTVLTFLLGMFSALVA
YFSPALGGILLQINSMLDGLDGEVARAQMRTTKFGAWLDSVLDRYVDFAFLSALAMHL
KPSWDFMPWYFAALFGSVWVSYSTERYKGAYCEDAYAVIKELRYLLGKRDERIFMIMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'translation="MVETAVILAGGEGNRLKPLTEBVPKALLKVAGRELLYRTIKQLO
)VGVKNFVIVVNKKFEGKVKAFLKEHNPEAEVIPNEHPEKENGYSLYLAKGRIKGEFA
)VMSDHIYEKAFLEKAVEGKGLIVDRLGLYINKNEATKVKCEEGRIKYIGKNLEKYDG
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Nalkgkkgvypyehraelvrsikyvdlvipernwegkiedikkynvdyfvmgddmkgk
PDYLKEYCEVVYLPRTEGISTTELKEALVKLSNILEEDILRVLDIVVRGRICIEEILK
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EEMMKKMVRYPRVVVYSSDVLTYIKDIYPDVQSKAYVIAREIAKETGSAPELEELGKI
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                                                                                                                                    2 (bases 1 to 15820)
Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,
Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M.,
Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product="glucose-1-phosphate thymidylyltransferase"
protein_id="AAC07344.1"
db_xref="GI:2983786"
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protein_id="AAC07343.1"
db_xref="GI:2983785"
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/product="rare lipoprotein A"
/protein_id="AAC07342.1"

    15820
    organism="Aquifex aeolicus"

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                                   (6674), 353-358 (1998)
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complement(1313. .1819)
/gene="tagD2"
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/gene≂"spsI"
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complement(12. .1298)
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/gene="aq_1369"
1794. .2576
/gene="aq_1369"
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transl table=
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/gene="rlpA1"
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'gene="rlpA1"
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AAGGCTCTTTACTTCGGCAGAGGTGACTTAATTCCCGGTGCTTCTCGGAAGTTGTTCCATA
                                AGGGCTCTATACCTCTCGGAAGGGAGTTTAATCCCCGCACTTCTCGGCAGCTGTGCAATT
                                                                                                                                                                                                                                                                                                                                        GGGATGTTCAGCCTTCTGAAGAGGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCGCCCATATAGGTGTTTTAAAAGCTCTGGAAGAGCTCGGTATAAAGGTAAAGAGGCTC
                                                                                                                              AGGAGAATAGAAAAACTTGAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGA
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DGFINALYKYFFKFVKFLMKYLDIKIIDVLIHETVLTAFRLGRLSRRLQTGLVNHYIL
:FLAVGLTFILGIMLYILDRL"
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FFKALLFLAAGAVITAFHHHLYDIFKMGGLKKYMPVTYVAFMIGALSLAGVFPFSGFW
SKDRIVASMYEWSGVLGVLGTIVAFITAYYAFREGFLVFHGRERWREIYDKDVHEVEG
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ATKASFEAFVMNRIGDWLFIFGIIYSFYLFKTLEITQIFPKVEEVDKYALGVATMLLF
GGAVGKSGQFFLHTWLFNAMAGPTPVSALLHAATMVAAGVYMVARLYFWFEATPQTLK
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IFFTAGAELVGALQLLIYAVAIAVFYIIVISAVFWEKAKKSESHYRFEGLISLFVVLF
LYIEMIVVFLLGVKASPEGKIAKFIEKFGNTEVIGAILFSKYFLAFEVVSIVLLMGMI
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LVVALKAIHSPIHVKLYDFLPIGNYTLSLGFYFDSLSSLMALVVTFVATLIFVYSIGY
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/codon_start=1
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/note="aq_1379"
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NIALVGADHYLGLAEGQIFALFIIALAATEAAVGLGIIIAIFRLKKVESTDEIRELRG
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/transI_table=1
/product="NADH dehydrogenase I chain
/protein_id="AAC07351.1"
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/db_xref="GI:2983792"
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/product="NADH dehydrogenase I chain
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5743. .7051
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Pred. No. 4.8e-110;
0; Mismatches 209;
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                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 11357)
Eisen,J.A., Nelson,K.E., Paulsen,I.T., Heidelberg,J.F., Wu,M.,
Eisen,J.A., Deboy,R., Gwinn,M.L., Nelson,W.C., Haft,D.H.,
Dodson,R.J., Deboy,R., Gwinn,M.L., Nelson,W.C., Haft,D.H.,
Hickey,B.K., Peterson,J.D., Durkin,A.S., Kolonay,J.L., Yang,F.,
Holt,I., Umayam,L.A., Mason,T., Brenner,M., Shea,T.P., Parksey,D.,
Nierman,W.C., Feldblyum,T.V., Hansen,C.L., Craven,M.B., Radune,D.,
Vamathevan,J., Khouri,H., White,O., Gruber,T.M., Ketchum,K.A.,
Venter,J.C., Tettelin,,H., Bryant,D.A. and Fraser,C.M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eisen, J.A., Nelson, K.E., Paulsen, I.T., Heidelberg, J.F., Wu, M., Dodson, R.J., Deboy, R., Gwinn, M.L., Nelson, W.C., Haft, D.H., Hickey, E.K., Peterson, J.D., Durkin, A.S., Kolonay, J.L., Yang, F., Holt, I., Umayam, L.A., Mason, T., Brenner, M., Shea, T.F., Parksey, D., Nierman, W.C., Feldblyum, T.V., Hansen, C.L., Craven, M.B., Radune, D., Vanathevan, J., Khouri, H., White, O., Gruber, T.M., Ketchum, K.A., Venter, J.C., Tettelin, H., Bryant, D.A. and Fraser, C.M. The complete genome sequence of Chlorobium tepidum TLS, a photosynthetic, anaerobic, green-sulfur bacterium proc. Natl. Acad. Sci. U.S.A. 99 (14), 9509-9514 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlorobium tepidum TLS
AE012939 AE006470
AE012939.1 GI:21647896
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                                                                                                                                                                                                                                                                                                           Submitted (30-APR-2002) The Institute for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlorobium tepidum TLS.
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                                                                                                                                                                                                                                                                  unpublished
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                                                                 complement (75.
/gene="hsdR"
/note="identified by match to TIGR protein family HMM
TIGR00348"
                                                                                      /note="CT1878"
                                                                                                                                  complement (75.
                                                                                                        gene="hsdR"
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                                                                                                                                                                              strain="TLS"
                                                                                                                                                                                                   organism="Chlorobium
                                                                                                                                                                                                                                             ocation/Qualifiers
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                                                                                                                                                       _xref="taxon:194439"
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                                                                                                                                                                                                                                                                                                              Research,
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KOPAATEPOKHTILSTYJULHYSVDOSSTILLYNREPYQLAATER LIMIKIKSSHQKTWST

PEGGGTI WHTTGSGKTLITSFKAARLGTELDET DKVEFVVDRADLESTYMKKIKSSHQKTWST

SVNGSDSTAGLKRULEKDDRI II VIT OKLINILMKSEPDL.PI YHKQVVPI FDECHRSQ

PERAQENSTAGLKRULEKDDRI II VIT OKLINILMKSEPDL.PI YHKQVVPI FDECHRSQ

PERAQENGLRKKEPRYLEFEDDEKKLSAAENTAGAPFREELSTYTKOVPI I FDECHRSQ

PERAGENSTALPANSVBARKLSAAENTOGOSSTAFTRESTYTTTATAGATHA

ADEGFEVSALNSSAKEFLNAALLYPERTOGOSSTAFTRESTYNILTERVATTE

RELPADLEQATI DAJITLGENKTNRYVLEKSYREYMGGTOGOSRKGFYTP

BLOAREPPPAALEKEADKKAFVRILGESTLRAENVOLDERSYTTAALTGORKRYFTP

BLOAREPPPAALEKEADKKAFVRILGESTLRAENVOLDERSYTTAALTGORKRYFTP

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EAFKAQHYLSDBDLAALQAIKLIPPERTMQDYRSTYNDIRDWILREQAGVEKEKSTIDW
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AKDVLRNLEGTVEFLKOHPALTGTPPERGNKTALTGTPPERGNKTALTGTPPERGNKT
ALTGTPPERGNKTALTGTPPERGNKTTLTEARE"
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GVGCIHYQUTHTYGYWTTEFKSPIDPEPANRIKKARRCBDJVIATTSEDDDAVAKAVA
MIGTEDVAVSTDAYIFANDKYMSYFPQTDMFQEQKKPYITGTKVRRISGDNIAKI
LIPIPPLAEQERIVATLLOQPDALTNSITEGLPREIELRQKQYAYYRDLLFSFPKASFG
GVPEGRDQFPSFGGVPEGGGLAA"
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                                                                                                                                                                                                                                   SGGEQLWDQFPSFGGVPVGRGGYNRYDVTILVNGLPLVQVELKRGVAIREAFNQVHR
YSKESFNSAHSLFKYLQLFVISNGTDTRYFANTTRRDKNSFDFTWHWAKADNTPIRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDVVFEVDLLKSQEINLÖYILELIFBRNKETRSKAELVEEVRRVIRASLGHRAKESLV
VDFINQTDLEQLADKASVIEAFFTFARAELQREAQELIEAEKLNAEAARRYIATSLKR
EFASDTGTDLNAVLPRMSPLNPQYLTKKQSVFQKIAAFVEKFKGVGGQV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="identified by Glimmer2; putative"
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//transI table=11 /gene="CT1883" /note="identified by Glimmer2; putative" /note="identified by Glimmer2; putative" /product="glycosyl transferase" /protein_id="AAM73101.1" /db_xref="G1:21647901" /product="hypothetical protein" /protein_id="AAM73103.1" /db_xref="G1:21647903" complement (9871. .11253) complement (8408. .8875) complement (7106. .8236) complement (7106. .8236) complement (9084. .9866) complement (9084. .9866) complement (8408. .8875) db_xref="GI:21647902 complement (9871. /codon_start=1/transl_table=11 /codon_start=1 /transl_table=11 /codon_start=1 /transl_table=11 8875. .9003 /gene="CT1884" 8875. .9003 /gene="CT1884" /gene="CT1883" /note="CT1886" /gene="CT1882" /codon_start=1 gene="CT1882 /gene="CT1885 qene="CT1885 gene="aldA ARIEGEEDEA" gene="aldA PF00534" PF00171"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Hickey, M.J., Brinkman, F.S.L., Hufinagle, W.O., Kowalik, D. Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrook-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Swong, G.K.-S., Wu, Z., Paulsen, IT., Reizer, J., Saier, M.Hancock, R.B.W., Lory, S. and Olson, M.V.
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Thermoanaerobacter tengcongensis strain MB4T, section 163 of 244 of the complete genome.
AE013136 AE008691
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3727 c 3693 g 1799 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRFHQFQYFGLISPELIGGČALAQLSLLGVGFVYLYQPSSGRMLERRFKLPLGFGTRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MQRLIQANGQPHYGIFPSAPQHINYRDFDFRSPMGRRVGALGKW
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abo(2., Tan, X., Tan, Y., Tan, Y., Yang, J.,
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Tan, H., Chen, R., Wang, J., Yu, J. and Yang, H.
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Bacteria, Firmicutes, Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
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complement(9796. .10965)
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                                              complement (8629. .9645)
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PPLSGYGTTDFGRVPQLIDAGYRATTVLAARLAELRERKENDLSEALLDVARTBNGRKPV
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KLNTLVTHATGKKGGTPPLRLGLINLSDDMRGESTPRLGGSYRMNGLNRLGABRLTRVQ
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IGGARRELSGPRRDALSGQNYSLGRIVYTRRLTERSFLDDFPLYLGSSIERGRIWNN
NEYDSGYINAASLMIGFDFDFLYFSYGINDENFKAFYLNLGGNF"
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SQVVGLRYFWYGYERFHKGRWASVAYYCQLRRDGRVELFGEHGGFPPGGHLRDFV
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product="probable transcriptional regulator"
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358. .5744
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/transl table=11
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protein_id="AAG06728.1"
/db_xref="G1:9949472"
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complement(8077..8511)
/gene="PA3341"
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/gene="PA3340"
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Submitted (07-OCT-2001) Institute of Biophys Sciences, Beijing 100101, China
4 (Dases 1 to 11618)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Sciences, Beijing 100080,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tian,Y., Xue,Y., Xu,Y., Lai,X., Huang,L., Dong,X., Ma,Y. and Tan,H Direct Submission
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                 /note="TE1839"
complement(1501.
                                                                                                                                        complement (637. .1485)
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baielaasigadiiincdvsssidmgfperppyslansekvlpikkypnikrplpbii
                                                                                                                                                                                                                                                                                                                superfamily"
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                                                         complement (1501.
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protein family UPF0028, score 39.6, E-value 2.80E-12"
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|strain="MB4T"
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/note="Best Blastp hit = gi|7517111|pir||C72463
hypothetical protein APE2350 - Aeropyrum pernix (strain KI) gi|51106052|db|BaA81363.1| (AP000064) 231aa long hypothetical protein [Aeropyrum pernix], score 60.5,

.00E-08"

complement (4233. .4979) /gene="PncA"

'note="TTE1842"

complement (4233.

.4994)

complement (4146.

.4150)

/gene="TTE1841"

MQNTEK"

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/codon_start=1 /transl_table=11 /product="conserved hypothetical protein" /protein_id="AAM25032.1"

ınknown [Bacillus halodurans], score 70.5, E-value

(AP001516) BH2709

.00E-12"

note="Best Blastp hit =

gi | 10175330 | dbj | BAB06428.1 |

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/gene="AarF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Pfam match to entry tetR, Bacterial proteins, tetR family, score 67.4, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein 4 - Clostridium pasteurianum pila11950 emb|CAA82211.1| (Z28353) similar to a B.s gene (GB: BACHEMEHY 5) [Clostridium pasteurianum], 64.3, E-value 1.00E-09"
                                                                                                                                                                                                                                                                                                                                                                    /trānslation="m@HlrryreiifvfikygfgaiidnigiikHinvrrkiik@Tnd
Enlaklsrgerlrlaleelgffikm@jilstrsdiirediikelekl@krapafsfi
EvksviQnbrgesleeayabreffplaaasiayovHkallwsGkttvvvkyQrpgteki
AQDMRILBDIAkfvDNHTKYGKIYNFTKMVEDFKKRLEEELDFRIEGENAEKFKKNFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (2100. .3788)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (2080. .2084)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (1903. .2043)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MFGTGIQVILDSNENEILDALNAIQIIFE"
                                                                                                                                                                                BSIIDLNAVTLANMKKLEKDINNLÆDRYVBIPLEKLKVGEVLNGIFPLLVFSYNIVIP
NEFNNLAKSLITLEGIVEKLDEVAKFIRKJELFKRYDKYSTQHMKEBIINATMDY
SRLIKELBSFLLNFIRKTEBENYAIELKIRDLENLEKRVDKVENRLSTSIILLALSIV
IAGILIGSGMSANAGAEMYKLNGIILKIGLAIAFVIVLGLAISIFRSGRL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="megknosorilnaaykcistkgyanvslrdiaeeagvvlsolhy
yfgskeglftevikmminkylkeinealsmgetakdkmlslvnffkdllknnpglfkl
lydftglammsssensllkdlfndlskmieekilsnsalgenfrnyspravarmilga
complement (3811. .4137)
/gene="TTE1841"
                                                                                           complement (3811.
                                                                                                                                                    complement (3784. .3788)
                                                                                                                                                                                                                                                                                                                                    KDKKVKI PSI I WTHTTRRVL TMBY I GG I PLNDFNA I DEAGLDRGA I ARNLAKSVLNQ I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Transcriptional regulator"
/protein_id="AAM25030.1"
/db_xref="GI:20516854"
                                                           /gene="TTE1841"
                                                                                                                                                                                                                                                                                                        LRDGFFHGDPHPGNIMVLEDGTIAFLDFGMVGSLSPERKRQFSKMLLGIVYKNSRMII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'product="predicted unusual protein kinase"
'protein id="AAM25031.1"
'db_xref="GI:20516855"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Best Blastp hit = g
(AP001516) ABC transporter
§73, E-value 1.00E-102"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="TTE1840"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="AcrR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Best Blastp hit = gi|481591|pir||S38906
                                                                                                                    gene="AarF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="AarF2"
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                                                                                           .4150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 - Clostridium pasteurianum
11.1 (Z28353) similar to a B. subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gi|10175329|dbj|BAB06427.1|
r [Bacillus halodurans], score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulatory
3.00E-16"
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37 24-1999 arotovora subsp. carotovora subsp. carotovora subsp. carotovora expL, expM, and galU genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVPVSLARAMGADIVIAVDLOHDASLNHQDLLSIKPTASEVDIDMEHYSQDWRSRIRE
RLLRGRRQSAESSPTAMEIMSTSIQILENRLKMTRMAGDPPDVLLQPYCPQIATLDFH
RAQEAIEAGYKAVAKMRDELLPLATEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SILEHYHPDIMICDLKMPMWGGIEFLECLRLKDSDTPILVISATSQMADIAKVLRLGV
QDVLLKEIRDNYTRLRDAVWSCLYPDMFTSQLADELDQMAQDMSLLNQSPRAITKLLAQU
QPPVQQTLARCRVWYRQLTTARQDGIVLDIAALSETELAFYCLDVTGGVNNNGTLAAL
LLRTLFNGLLQBHLVDQQHRLPYLPTLLKQVNQLLRQASLDGRPPLLVGYYHRPLKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVGAAYATENILSSNEOWVRGFGYWDVIRLMDLSWQRGSLLRGDRVFNSVKHLLHTTQI
EDCAIKYGVVTTNLSTGRELWLTEGDLHQAMRASCSMPGLLSPVRFNDYWLVDGAVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'translation="MQRKKIGIALGSGAAKGWAHIGVFNALAELGIDVDVVAGCSIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'translation="MEQPLAGKHILVIDDEAVFRSVLAGYLTSLGASVREAINGLDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'organism="Pectobacterium carotovorum subsp. carotovorum"
                                                                                                                                                                                                                                                                     expL gene; expM gene; galU gene; response regulator.
Pectobacterium carotovorum subsp. carotovorum.
Pectobacterium carotovorum subsp. carotovorum
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                            The response regulator expM is essential for the virulence of Erwinia carotovora subsp. carotovora and acts negatively on the signa factor RpoS (sigma s)
Mol. Plant Microbe Interact. 12 (7), 575-584 (1999)
99407916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-MAR-1998) Andersson R.A., Plant Biology, Swedish University of Agricultural Sciences, Box 7080, 750 07 Uppsala, SWEDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Function="regulation of virulence factors"
                                                1052 TGGAGTACAATGGAACCAAGTTAGTTGATGGATCAATTGTTGA 1010
440 ITGAGTATAAGAATTACTTGCTCGTTGACGGAGGTATAGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                       Andersson, R.A., Palva, E.T. and Pirhonen, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein id="CAA11942.1"
|db_xref="GI:3319928"
|db_xref="SPTREMBL:086197"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein_id="CAA11941.1"
|db_xref="G1:3319927"
|db_xref="SPTREMBL:086196"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="ExpL protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="ExpM protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="rssA homologue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            evidence=experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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transl_table=
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/gene="expM"
1370. .1373
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/gene="expL"
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/gene="expL"
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gene="expM"
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gene="expL"
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                                                                                                                                                                                                                                                AJ224437.1
                                                                                                                                                                                                                       AJ224437
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                                                                                                                                                                                             DEFINITION
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                                                                                                                        RESULT 5
ECJ224437
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TITLE
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AUTHORS
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MEDLINE
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                                                                                                                                                                                                                                                                                               SOURCE
                                           요
ઠે
                                                             /protein_id="AAN25033.1"
/brotein_id="AAN25033.1"
/brotein_id="AAN25033.1"
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PPHCVKGFTFESEIVDELKEIIBPIKNLLKACYRAGIKNVPFGGELEGGNEFLKKVVEMIKA
GKSTPIVVGDCTDLCVYQTAASIKMIANANNLKVNVIVPENCVETYDTSVKTAQSLKI
NPHDGNLIHTWPLYHPRLAGIRGYVELLEE"

complement (4990. .4994)
                                                                                                                                                                                                                                                                                                                                                                                                             /note="Best Blastp hit = gi|11499845|ref|NP_071089.1|
conserved hypochetical protein [Archaeoglobus fulgidus]
gi|333444|sp|028020|xM64_ARCFU HYPOTHETICAL PROTEIN
AF2264 gi|7430238|pix||H65532 conserved hypothetical
protein AF2264 - Archaeoglobus fulgidus
gi|2648253|gb|AAB88986.1| (AE000948) conserved
hypothetical protein [Archaeoglobus fulgidus]
F-value 7.008-17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MKAINSGIDEKLPEDLIKVNRDTNFHQLIGVHVVELGGGYAVTE
INEBERGHINPLAIAHGGVLFSYMDITMGMAARTVGKQVITIEMNINYLSPVRVGEKVK
AKGKIVHAGSKTTVNVCEAYABDGRLLAVARETFFNVLD"
COMPLEMENT (5043. .5405)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Pfam match to entry DUF157, Uncharacterized protein Paal, COG2050, score 103.2, E-value 5.10E-27" complement (5468. .5472)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1472 TAGGACTTATACTGGGCGGTGGAGCAAGGATATGCGCACTTAGGTATACTAAAAA 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1352 TAGGAGCAATCTATGCTTCAGGACATAATGTAGACAAACTTATAAGTGATGCAAAAAAGA 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1172 ATATTCCTCTATATATTGTGGCTACTGATATTCAAACAGGAAGAAGGGAGTAGTTTAAAG 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1412 GATTTGAAGAAAATATTCCTATTGATTTTATAGTAGCATAAGTATGGGAGCGATAA 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1292 TTAATATGTTAAAATTTATAAGTTTTAGATTTTAAAGCCTCACGAACCGCTTAGTAA 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1112 AGGGAGACTTTGATAAAAGCTATAAGGGCAAGCATTTCTATCCCTGCCTTTTTTTGAACCTG 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGCTATAAGATTCCTTGAGGAAGTTCTCCCTTACAGG-----AGAATAGAAAACTTG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
/product="uncharacterized protein, possibly involved :
aromatic compounds catabolism"
/protein_id="AAM25034.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCATAGCCCACATAGGTGTTTTGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITCGGTCTTTTATGCCTCAGGCTACTCCCCTGAAGGGATGTTCAGCCTTCTGAAGAGGG
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                                           product="Amidases related to nicotinamidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 241; Indels
                                                                                                                                                                                                                                                                                          complement (5034. .5472)
                                                                                                                                                                                                                                                                                                                                                                    complement (5034. .5459)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="GI:20516858"
                                                                                                                                                                                                                                                                                                                                        'note="TTE1843"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="Paal2"
                                                                                                                                                                                                                                                                                                                                                                                           gene="Paal2"
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                                                                                                                                                                                                                                                                gene="PncA"
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Best Local Similarity 46.7
Matches 216; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Snoo
                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                        MEDLINE
                                                                                                                                                                                                                                                                                 TITLE
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Best Local
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1 (bases 1 to 329100)

Capela,D., Barloy-Hubler,F., Gouzy,J., Bothe,G., Ampe,F., Batut,J., Botlean,S., Gloux,S., Boistard,P., Becker,A., Boutry,M., Cadieu,B., Dreano,S., Gloux,S., Godrie,T., Goffeau,A., Kahn,D., Kiss,E., Lelaure,V., Masuy,D., Pohl,T., Portetelle,D., Puehler,A., Purnelle,B., Ramsperger,U., Renard,C., Thebault,P., Vandenbol,M., Weidner,S. and Galibert,F. Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meilloti strain 1021

Sinorhizobium meilloti strain 1021

Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9877-9882 (2001)
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Sinorhizobium meliloti 1021 complete chromosome; segment 6/12.
AL591787 AL591688
AL591787.1 GI:15074266
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   Laboratoire de Biologie Moleculaire des Relations
Plantes-Microorganismes, UMR215-CNRS-INRA, BP27, F-31326 Castanet,
France, Laboratoire de Genetique et Developpement UMR6061-CNRS,
Paculte de Medecine, 2 avenue du Pr. Leon Bernard, F-35043 Rennes,
France, GATC GmbH, Fritz-Arnold-str. 23, D-78467 Konstanz, Germany
                                                                                                                               Direct Submission
Submitted (26-JUL-2001) Gouzy
                                                                                               MELILO EU Consortium:
                                                                                                                EU Consortium
                                                                                                                                                                        Gouzy, J.
                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; al
Rhizobiaceae; Sinorhizobium.
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VVNECTAAGINETILVTHSS"
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/product="GalU protein"
/protein id="CAA11943.1"
/db_xxef="GI:3319929"
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2604. .>2797
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2593. .2597
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Pred. No. 3.2e-05;
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   Konstanz, Germany
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                                                  Gene name confidence : pu
predicted by Codon_usage
predicted by Homology
                                                                                                                                                           /gene="acpD OR SMc01329"
2063. .2683
/gene="acpD OR SMc01329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted by Codon_usage predicted by Homology predicted by FrameD"
                                   predicted by
                                                                                                                             biosynthesis"
                                                                                                                                                                                                                                 GLLPATRALIDFLAENLIKALERCREVDPRPAASFEI"
                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (914.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SMC01330"
'function'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
complement(373...798)
                                                                                                                                          'function="small molecule metabolism;
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'transl_table=11
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db_xref="GI:15074267"
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product="tRNA-Thr"
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                    start=1
                                   FrameD"
_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .798)
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Universitaet Bielefeld, Biologie IV (Genetik) Universitaetstr 25 D-33615 Bielefeld, Germany, Unite de Biochimie physiologique, Universite Catholique de Louvain, Place Croix du Sud 2, Bte 20, B-1348 Louvain-la-Neuve, Belgium, Unite de Microbiologie, Facult des Sciences Agronomiques de Gembloux, Avenue Marechal Juin 6, B-5030 Gembloux, Belgium. B-mail-Jerome Gouzy@toulouse.inra.fr http://sequence.toulouse.inra.fr/meliloti.html. Faculte

organism="Sinorhizobium meliloti" |strain="1021" ACA; predicted by tRNAscan-SE"

ERWYRRGDEEVGNRQFVVADPDGYLLRFYEPLGRRPRTS:" /product="CONSERVED HYPOTHETICAL PROTEIN"
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TPMLADILPAFHRRYFGWRLLITASNRRIDLIERERIDVALRARDQLDTDSQLTVRKFG
EVRQRLAASPTLARLGEITTDNLSQWPTLSWNEQHPNDVWRLVHATGGAIBIAHRPV
VGCSDFLILEEAAAIEGMGIALLPDHTCERAFRTGALVPVLPEWTSGNVMVHLVFPSRH

note="Product confidence : probable fatty acid

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3066. .3941)
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/function="macromolecule metabolism; macromolecule
fynthesis, modification; rna synthesis, modification , dna
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LOGYACLRRGDISYLARCEMMINVTTWKRLQDGCPTAGLAVTIVPSAPIP"
complement (3066. . 3941)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="MSKDKTGDKSARDTHYANLRRAHRDARRERGEIPTPRQDKRAKL
SADWKPPALAPDQVLLYGLHTVRAALDNPERRIIRLSVTQNAAARLDLGDLTALPFPT
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RETVAFDAGALITTWRHSPTESGVLAKSASGALELIPYIQITNLADTLEELHELGFWT
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AAAIAMYAARHHLKG"
product="PROBABLE ACYL CARRIER PROTEIN PHOSPHODIESTERASE"
                                                                                                                                                                                                                                                           /function="miscellaneous; hypothetical/partial homology"
/note="Product confidence : hypothetical
Gene name confidence : hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="PUTATIVE TRNA/RRNA METHYLTRANSFERASE PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="tRNA-Gly"
note="codon recognized: GGA; predicted by tRNAscan-SE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="tufB OR SMc01326"
/function="macromolecule metabolism; macromolecule
synthesis, modification; proteins and peptides -
                                                                                                                                                   VFGFPGITD1EFIRAEGLNLGPDQKQFAIAEABKTIAEGNVLKLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                        product="HYPOTHETICAL TRANSMEMBRANE PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Product confidence : putative
Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein_id="CAC45916.1"
db_xref="GI:15074270"
db_xref="SPTREMBL:Q92KB9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein_id="CAC45917.1"
db_xref="GI:15074271"
db_xref="SPTREMBL:Q92Q16"
                                                                                                                                                                                                                                                                                                                                                                                               evidence=not_experimental
transl_table=11
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evidence=not_experimental
trans1_table=11
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                  protein_id="CAC45915.1"
db_xref="GI:15074269"
                                                                                                                                                                                                                                                                                                                              predicted by Codon usage predicted by FrameD"
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predicted by Homology
predicted by FrameD"
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'gene="tufB OR SMc01326"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4158. .4242
/gene="tRNA-TYR_GTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266. .4339 _
gene="tRNA-GLY_TCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266. .4339 __
gene="tRNA-GLY TCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1158. .4242
/gene="tRNA-TYR_GFA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="tRNA-Tyr"
                                                                                                                                                                      2792. .3076
/gene="SMc01328"
                                                                                                                                                                                                                  2792. .3076
/gene="SMc01328"
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                                                                                                                                                                                                                                                                                                                                         /translation="MAKSKFERNKPHVNIGTIGHVDHGKTSLTAAITKYFGEFKAYDQ
IDAAPEEKARGITISTAHVEYETPNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVS
AADGPMPQTREHILLARQVGVPAIVVFLNKVDQVDDAELLELVELBVRELLSSYEFPG
                                                                                                                                                                                                                                                                                                                                                                                                                     DDIPIVKGSALAALEDSDKKIGEDAIRELMAAVDAYIPTERPIDQPFLMPIEDVFSI
SRGTVVYTSRYBKGIVKVGKEBIBIVATRPTKYTCTGVBMFRKLLDQGQAGDNIGALL
RGVDRNGVBRGQILCKFGSVKBHKFRARAYILTKEBGGRHTPPFTYVRPQFYERTTD
VTGIVTLPEGTEMVMPGDNVTVDVELIVPIAMEEKLRPAIREGGRTVGAGIVASIVE
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                                                                                                                                                                                                                                      /product="PROBABLE ELONGATION FACTOR TU PROTEIN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.3%; Score 55; DB 1; Length 329100; Best Local Similarity 46.0%; Pred. No. 4.4e-05; Matches 227; Conservative 0; Mismatches 260; Indels 6
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                           /note="Product confidence : probable
Gene name confidence : probable
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translation and modification"
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Sequence 561 from Patent WO9924578.
A96528
                                                                                                                                                                                                                                                         /protein_id="CAC45918.1"
|db_xref="GI:15074272"
|db_xref="SPTREMBL:Q925Y6"
                                                                                                                                                                                  /evidence=not_experimental
/transl_table=11
                                                                          predicted by Codon usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SMc01325"
6125. .6790
                                                                                                                                                            codon start=1
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Parkhill, J., Achtman, M., James, K.D., Bentley, S.D., Churche Klee, S.R., Morelli, G., Basham, D., Brown, D., Chillingworth, Davies, R.M., Davies, P., Devlin, K., Feltwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Moule, S., Mungall, K., Quail, M.A., Rajandream, M.A., Rutherford, K.M., Simmonds, M., Skelton, J., Whitehead, S., Spratt, B.G. and Barrell, B.G. Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
                                                                                                                                                                          Neisseria meningitidis Z2491.
Neisseria meningitidis Z2491
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
                                                                                                                                                                                                                                                                                        Neisseria meningitidis segment 1/7.
                                                                                                                                                                  Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO (IT); CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisserial antigens
Patent: WO 9924578-A 561 20-MAY-1999;
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Pizza,M., Scarlato,V., Rappuoli,R., Grandi,G. and Masignani,V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGATAGTCGGCAGCCTTTTTGCATCGGGTATGTCGCCCGACCGCCTCGAATTGGAAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                               GTTATCATCGGCAGGCATACATATGTTGACGGCGGTCTGTCGCAGCCCGTGCCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTGAGTATAAGAATTACTTGCTCGTTGACGGAGGTATAGTTAACAACCTTCCCGT 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAGGGAATGCCGGGCAGGCTGTGCGCGCCGCCCATTCCCAATGTGTTCCAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAATTTTAGGTAAAACCGATTTGGTCGATTTAACCTTGTCCACCAGTGGTTTTATCAAA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGAGGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTGATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAATCGTTTCGGTCTTTATGCCTCAGGCTACTCCCCTGAAGGGATGTTCAGCCTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGAAAGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTAAGCGGGGTGAGCGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGTGGTCGGTTTGGCACTCGGTGGCGCGCATCTAAAGGATTTGCCCCATGTAGGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAGAGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCATAGCCCACATAGGTGTT
                                                                                                                                            (bases 1 to 340806)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                     AL157959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:32644"
231 c 250 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="unidentified"
                                                                                                                                                                                                                                                       GI:7378778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.5%;
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                                                                                                                                                                                                                                                                                                                       340806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53.6;
Pred. No. 9.
                                                                                                                                                                                                                                                                                                        serogroup
                                                                                                      James, K.D., Bentley, S.D., Churcher, Casham, D., Brown, D., Chillingworth, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 264;
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                                                                                                                          Churcher, C.,
                                                                                                                                                                                                                                                                                                                       BCT 04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                    genome;
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AUTHORS
TITLE
JOURNAL
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MEDLINE
PUBMED
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            misc_feature
                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SdD
                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (30-MAR-2000) Submitted on behalf of the Neisseria sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 340806)
Parkhill, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Details of N. meningitidis sequencing at the Sanger Centre available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Notes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .0761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/N_meningitidis/).
                                                                                                                                                                                     /note="NMA0002, nuoL, NADH dehydrogenase I chain L, len: 674 aa; similar to many e.g. NUOL RHOCA NADH dehydrogenase I chain L (EC 1.6.5.3) (700 aa). Contains Pfam match to entry PF00361 oxidored q1, NADH-Ubiquinone/plastoquinone
                               NADH-Ubiquinone/plastoquinone score 351.80, E-value 7.3e-102
                                                                                                      complement (1116. .2030)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (complex I), various chains, and to entry PR00662 oxidored_q1_N, NADH-Ubiquinone oxidoreductase (corchain 5 N-terminus"
                                                                                                                                                                          NGIVNGSARLVGAVAAQVRKVQTGFIYTYAAAMVFGVLVLLGMTFWGLFR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (414.
                                                                                                                                         note="Core DNA
                                                                                                                                                             1035.
                                                                                                                                                                                                                                                                                                                                                                                     /product="NADH dehydrogenase I
/protein_id="CAB83322.1"
/db_xref="SWISS-PROT:Q9JX92"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein
/protein_id="CABB3321.1"
/db_xref="G1:7378779"
/db_xref="SPTREMBL:Q9JX93"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="NMA0001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="NMA0001"
                                                              note="Pfam match to entry PF00361 oxidored
                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1/
transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="nuoL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="serogroup:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EC_number="1.6.5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="nuoL'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="NMA0001, unknown,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MSNTQTIRSADFTTSRAWGALDIANMNGTTVRLHWTDQPYKWHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strain="Z2491"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Neisseria meningitidis Z2491"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (6777),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .340806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _xref="taxon:122587"
                                                                                                                                                           .1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     502-506
                                                                                                                                       uptake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (2000)
                                  7.3e-102"
                                                                                                                                       sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        len: 106
                                                 (complex
                                                                                                                                                                                                                                                                                                                                                                                                                                            chain
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                                                                                                                                     gccgtctgaa"
                                                 d_q1,
various
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chains,

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215050 CAAGGGAATGCCGGGCAGGCTGTGCGCCCTTCCGCCGCCATTCCCAATGTGTTCCAAACC 214991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215230 GAAATTTTAGGTAAAACCGATTTGGTCGATTTAACCTTGTCCACCAGTGGTTTTTATCAAA 215171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215110 CCCATCAAATTTGCCGCCGTTGCTACTGATTTTGAAACCGGCAAGGCCGTCGCTTTCAAT 215051
                        /note="NMA0006, muoJ, NADH dehydrogenase I chain J, len: 223 aa; similar to many e.g. NUOJ RHOCA NADH dehydrogenase I chain J (EC 1.6.5.3) (202 aa), fatsa scores; E(): 9.76-21; 41.3% identity in 201 aa overlap. Contains Pfam match to entry PF00499 oxidored q3, NADH-ubiquinone/plastoquinone oxidoreductase chain 6"
                                                                                                                                                                                                                                                                                                                                                               LWMLMQARFLGVTLVVVYYGAVMVLPLFVVMMLNIDIREMRAGFWRHAPVAGVGTLL
AVALILILVWPKTDLAÅFGLMKDIPADYNNIRDLGSRIYTDYLLPPRLAAVLLLLGMV
AAIALVHRKTVWPKRMDPADQVKVRADQGRMRLVKMBAVKPQTBSARBSBVSDDLKPK
                                                                                                                                                                                                                                                                                                                                         translation="MTFQLILFYIFAVIILYGAIKTVTAKNPVHAALHLVLTFCVSAM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 GAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 GCAATCGTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAAGGGATGTTCAGCCTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGAAAGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTTAAGCGGGGGTGAGCGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215350 ATTAAGGTTTTGAAAGAAACGTATTCCTGTGAAGGTGGTTACCGGCACATCGCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Pfam match to entry PF00499 oxidored_q3, NADH-ubiquinone/plastoquinone oxidoreductase chain 6, score 7.0, E-value 2e-19" complement(4570. .5277)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 AAGAGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTGATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 TGGGAGAAGGCTATAAGATTCCTTGAGGAAGTTCTCCCTTACAGGAGAATAGAAAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGGGAGTTTAATCCCCGCACTTCTCGGCAGCTGTGCAATTCCCGGCATATTTGAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215410 GCAGTGGTTTGGCACTCGGTGGCGCGCATCTAAAGGATTTGCCCATGTAGGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215170 GGCGAAAAGCTGCAAAATTACATCAACCGAAAAGTCGGCGGCAGGGGGATTCAGCAGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 340806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                           /cransl table=11
/product="NADH dehydrogenase I chain J"
/protein id="CABB3326.1"
/db_xref="GI="STR784"
/db_xref="GI="STR784"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /commal_table=11
/product="hypothetical protein NMA0007"
/protein_id="CAB83327.1"
/db_xrefe="GI:7378785"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="NMA0007, unknown, len: 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.1%; Score 53.6; DB 1;
14.5%; Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (3874. .3879)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="nuoJ"
complement (4034. .4525)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (4570. .5277)
     /EC_number="1.6.5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="NMA0007"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="nuoJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 44.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="NMA0004, unknown, len: 191 aa; similar to.
hypochetical proteins e.g. Y977 HAEIN H10977 (191 aa),
fasta scores; E(): 0; 80.5% identity in 190 aa overlap,
and to proteins involved in cell cycle e.g. TR:054679
(EMBL:AF036487) Lactococcus lactis Plasmid pNZ4000
putative mobilization protein (200 aa), fasta scores; E():
0, 55.1% identity in 167 aa overlap, and FIC_ECOLI cell
filamentation protein FIC (200 aa), fasta scores; E():
0.093, 29.4% identity in 126 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MPSENPIGKTMKSIDEQSLHNARRLFESGDIDRIEVGTTAGLOO
THRYLFGGLYDFAGQIREDNISKGGFRFANAMYLKEALVKIEQMPERTFEEIIAKYVE
MNIAHPFLEGNGRSTRIMLDLVLKKNIKKVVNWQNVSKTLYLQAMERSPVNDLEIRFL
                                                                                                                                                                                                                                                                                                                                                         /trānslation="MMDKNQLEQEFHKAMLNIYQEALNLPQPYKATRFLQIYNEFGGK
RAADKLLSTGEKKTQTGFTELILSGGGVHALKYSMEYLVLQKPWCDLFTEEQLAVARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mitlifituingallfgisamgifmnrknvivilmsielmllavn
fnriarsqhlgdiagqifvffvlivaaassaiglaimvlvyrnrqtinvadldbikg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="NAMA0005, nuok, NADH dehydrogenase I chain K, len:
101 aa; simlar to many e.g. NUOK RHOCA NADH dehydrogenase
I chain K (EC 1.6.5.3) (102 aa), fasta scores; E():
1.1e-24; 65.0% identity in 100 aa overlap. Contains Pfam
match to entry PF00420 oxidored_q2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       match to entry PF00420 oxidored q2,
NADH-ubiquinone/plastoquinone oxidoreductase chain 4L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Pfam match to entry PF00420 oxidored_q2,
NADH-ubiquinone/plastcquinone oxidoreductase chain 4L,
score 141.50, B-value 1.5e-38"
complement (3863. .4534)
                  NADH-Ubiquinone oxidoreductase (complex I), chain
N-terminus, score 77.20, E-value 3.5e-19"
complement (2487. .2828)
  entry PF00662 oxidored q1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="NMA0004"
/note="Core DNA uptake sequence: gccgtctgaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product=hypothetical protein NMA0004"
/protein_id="CAB83324.1"
/db_xref="G1:7378782"
/db_xref="SPTREMBL:09:no@"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="NADH dehydrogenase I chain K"
protein id="CAB83325.1"
/db_xref="GI:7378783"
                                                                                                                                                                                                                                                    product="hypothetical protein NMA0003"
protein id="CAB83323.1"
|db_xref="GI:7378781"
                                                                                                                                                      /gene="NWA0003"
/note="NWA0003, unknown, len: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKDNLTDDVDNRBIIFKGIEQSYYYEGYEKG"
complement (3516. .3525)
                                                                                                                                                                                                                                                                                                                               db_xref="SPTREMBL:Q9JX91"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="NMA0004"
/note="NMA0004, unknown,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="NMA0004"
complement (2952. .3527)
                                                                                                                           complement (2487. .2828)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .3527)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (3561. .3866)
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complement (3863. .4534)
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match to
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                                                                                                /gene="NMA0003"
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                                                                                                                            AE002562 9831 bp

Meisseria meningitidis serogroup

of the complete genome.

AE002562 AE002098

AE002562.1 GT:7227392
                                           Bacteria; Proteobacteria;
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Patent: WO 9924578-A 559 20-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unidentified
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N SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         559 from Patent
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Pred. No. 0.00028;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-MAR-2000) The Institute for Genomic Medical Center Dr. Rockville, MD 20850, USA Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MSRHPAPTGEKTFFGHPFQLSTLFHIELMERFSFYGMQGILLIY LYYTADKGGLGIDKTLAGGIVGAYSGSVYLSTILGAWFADRVMAEKTLFLSGIVVML GHIVLAAAPGLYGLLIGLIFIALGSGGVKSTASSMVGALYEQDEMRPLRDAGFSIFI AINIGGFLGPLLTGLLQENIGFHYGFGAAAVGWAFGLWRYSLGKKNLPHPTVPHFLSK GQGKTAAAVGIALIAALATAIKTGLVNLDNFSGILLSTVILAVIAYFARLLTNPRVSS
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WVILESGLMAAMWTKMGRKQPKTPLKEAMAVEVTGASFLGEVPEISSGTPMPIAVEAL
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                                                                                                                              complement (3122.
                                                                                                                                                                                                                                                                                                                                                                                                                                       DEIGFYRLLFYIGAATGFLLLLLVPKLNKMLEGTD"
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                                                                                                                                                                                                                                                                                                          putative'
                                                                                                                                                                                                                                                                                                                                                                                            /gene="NMB2137"
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                                                                 gene="NMB2138"
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                  SP:P28353 PID:154276 percent by sequence similarity;
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IMERSTYQLIAEVĀQIPDIPDIHYSNOSKYPESPĀĀFIROYRYDVTDDIHEĀETĀLJI
WRNARDDVHYQTLOGEDWMLLBIMGFSALSFDTLAQTLVEFMPEDDNWKNILLIGKWSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5101 GCAGTGGTTTGGCACTCGGTGGCGCGCCATCTAAAGGATTTGCCCATGTAGGTATT
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                                                                                                                               /note="conserved hypothetical protein; identified by Glimmer2; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to GB:L42023 SP:P45215 PID:1007577 PID:1221603 PID:1205695 percent identity: 66.11; identified by sequence similarity; putative"
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Pred. No. 0.0003;
0; Mismatches 265; Indels
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db xref="G1:7227401"
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(gnaagavraaaalipyvgpytigrhyydgglsgpypysaarroganyiladisak
PGKNISQGFFSYLDQTLANWSYSALQNELGAADVIKPQVLDLGAVGGPDQKKRAIRL
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FPPPFNLLPDALNWNLAMYAELLLPVLLLLGLATRLSALGLMVVTAVAWAAVHAGSGY
NVCDNGYKWALIYIVVLIPLLFQGAGGWSLDTLLKKRFCPRCRLKQD"
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:KSAEGSCGAAGSKAGEGKCGEGKCGATVKKTHKHTKASKAKSAEGKCGEGKCGSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="conserved hypothetical protein; identified by Glimmer2; putative"
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                     producE="peptide chain release factor 2"
protein id="AAF42446.1"
db_xref="G1:7227395"
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|trans1_table=1.1
|producE="conserved hypothetical protein"
|protein_id="AAR42447.1"
|db_xref="GI:7227396"
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|product="hypochetical protein"
|protein_id="AAF42449.1"
|db_xref="G1:7227398"
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protein_id="AAF42448.1"
db_xref="G1:7227397"
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db_xref="GI:7227399"
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/gene="NMB2141"
6088. .6396
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/translation="MPSEPGKNMIQHAGLGYRRDLAEDFLSLSENSPICFIEAAPENW LKWGWARKCPERVARELPLALHGLSMSLGGQAPLDTDLIDGIKEMMERYDCTFFSDH LKWCGHLYDLLPLPFTERWYHTPARRIREVQDRLGCRIAVENTSYTHSPLAEMN EVBFLMAVAREADCGHLDVNNIYVAAVNHGLLSPEAFLERVDAERKCYHTAGHDVB TPELLIDTHGAAVLPTWWDLLELAYAKLPTIPPTLLERDFNFPPFSELEAEVAKIADY

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319 GAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCCG

379 GAAGGGAGTTTAATCCCCGCACTTCTCGGCAGCTGTGCAATTCCCCGGCATATTTGAACCC 438

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Sequence 114 from E
AX044035
AX044035.1 GI:1134
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 GTTGAGTATAAGAATTACTTGCTCGTTGACGGAGGTATAGTTAACAACCTTCCCGT
                             CAGGGGAATGCCGGGCAGGCTGTGCGCGCCGCCCATTCCCAATGTGTTCCAACCC
                                                                                     CCCATCAAATTTGCCGCCGTTGCTACTGATTTTGAAACCGGCAAGGCCGTCGCTTTCAAT 153441
                                                                                                               GAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCG
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                                                        GAAGGGAGTTTAATCCCCGGCACTTCTCGGCAGCTGTGCAATTCCCCGGCATATTTGAACCC 438
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/db_xref="taxon:487"
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Takami, H., Masui, N., Nakasone, K.
Replication origin region of the
Bacillus halodurans C-125
Biosci Biotechnol Biochem. 63 (
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Takami, H., Takaki, Y., Nakasone, K., Sakiyama, T., Maeno, G., Sasaki, R., Hirama, C., Fuji, F. and Masui, N.
Genetic analysis of the chromosome of alkaliphilic Bacilly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic Bacillus sp. strain C-125 Biosci. Biotechnol. Biochem. 63 (2), 452-455 (1999)
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Sequencing of three lambda clones from the genome of alkaliphilic Bacillus sp. strain C-125
Extremophiles 3 (1), 29-34 (1999)
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Bacillus
AP001516
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Takami,H. and Horikoshi,K.
Analysis of the genome of an alkaliphilic
                                                                                                                                                                                                                                                                        Genome analysis
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Reidentification of facultatively alkaliphilic Bacillus sp. C-125
to Bacillus halodurans
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An improved physical and genetic
Bacillus sp. C-125
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Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                         halodurans
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halodurans genomic I
BADDOOOA
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16087 TGGCTTTAGGGTCAGGTGGAGCTCGTGGGTATGCACATATCGGTGTGTTGAAAGTATTAG 16028
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CVVIGVSNRVEIWSKELWEEYFABESEESFSEIAENIVDFDL"
                         TIMNHSLOYLNI SPSYBELKDEBERGYBLADFIGESARSARRELBOAGMKVYVLGEGD
TVEGQOPYSCHKLLEGERVILRTESESYTLPSMIGWSLRDVLKVANVLDVNVNLFGGG
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AFEBALLEAALDLTAFKGRICVITFHSLEDRICKEMFREASKGPDVPPGLPVIPEBYKA
TLKLITKKPIVPTAEEIELMNRARSAKLRIAEKQ"
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RKRIASBAGINKETLAKWLATVFRSLPBTEHTLDLYERVKTLAGRSNTYTDFPAELLL
      QVRNPDGPGYLNGHGKNI FSF1GMAPKDDPSVI VYVAVDRPSLNTNQVGSEPVAKI PN
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Aksigmkledenvkvvqn"
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/gene="BH2575"
/note="BH2575
                                                                                                                   complement (4529. .4891)
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/gene="BH2575"
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/gene="BH2577"
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/note="BH2574
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RLTIDSRVQTIIRRELDIARATYSPDGAIAIAMNPWTGRILGANSRRHYNPERFREVP
PEVYNQNKFIMQYSPGAFKIITLAAALESHEVDLTNDRFHDGFIEVAGHRLRCWK
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FRANDRIGFLEVATAFGGQGVSVTPIQQVAAVSAANNGGYLXEPYVAKDWVDFYTGEVV
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BPAKTGNDYYLTLDSNIQTALDQVMTQVEEBYKPERIIAIVADPKTGQILAMSNRPTF
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LPNEAASVYKKGALRAASTAFGQGTAVTPIQOIQAMTAIANDGKMKEYYVDRIUDS
ETGEVIEEKEPEVVGEPISKETAKEVRDILETVVTSSSGTGRPPYLEGFDVAGKTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and Technology Center, Deep-sea Microorganisms Research Group; 2-15 Nateushima, Yokouka, Ranagawa 237-0061, Japan (E-mail:takamih@jamstec.go.jp, URL:http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html, Tel:81-86-67-3895, Pars.81-468-66-6364)
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LENNHI VSFI GFAPADDPQI VVYVAI DNPKDTVQFGGVVAAPI VGKI I GDSLQALGI B
KRENQI EKERKWNDEPLVEVPDLVGRTKRDLHESYYELKI DADGKGDVVVAQAPEPGT
Nakasone, K., Masui, N., Takaki, Y., Sasaki, R., Maeno, G., Sakiyama, T., Hirama, C., Fuji, P. and Takami, H. Characterization and comparative study of the rrn operons of alkaliphilic Bacillus halodurans C-125
Extremophiles 4 (4), 209-214 (2000)
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LLABHINMSEERLLELLTRDVYQVELGAGARNLTQEQRDKIADLDLPGIYPTEEPRRY
                                                                                                                                                                                                                                                                                                                     Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis Nucleic Acids Res. 28 (21), 4317-4331 (2000)
                                                                                                                                                                                                                              Takami, H., Nakasone, K., Takaki, Y., Maeno, G., Sasaki, R., Masui, N., Fuji, F., Hirama, C., Nakamura, Y., Ogasawara, N., Kuhara, S. and Horikoshi, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="stage V sporulation protein (soprulation specific penicillin-binding protein) (spore cortex)" /protein id="BAB06291.1"
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organism="Bacillus halodurans"
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'db_xref="GI:10175194"
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/note="alkaliphile"
complement(179. .2113)
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/transl_table=11
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note="BH2573"
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Takami, H. and Takaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="spoVD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="spoVD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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AE005340
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 ATATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCGGAAGGGAGTTTAA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 40
21074935
                                                                                                                                                                                                                              Submitted (22-OCT-2000) Laboratory Wisconsin, 445 Henry Mall, Madison, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, B., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A., and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch P.A., and Blattoor P.S., Lin, J., Yen, G., Schwartz, D.C., Welch P.A., and Stroot P.S., Lin, J., Yen, G., Schwartz, D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli O157:H7 EDL933
Escherichia coli O157:H7 EDL933
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AE005340.1 GI:12514944
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Escherichia coli O157:H7 EDL933 genome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409 (681)
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Welch, R.A. and Blattner, F.R.
                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perna, N.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGAAGCTGTGCGGCCAAGCATTGCGATTCCCGGTATTTTTGTTCCGAAAAAACATAAACG 15668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGG 15604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCGACTGCTCATTGACGGCGGCGTTATTGACCGTGTACCTGTCTCTGTCGTCAAGGAGA 15608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCCCGCACTTCTCGGCAGCTGTGCAATTCCCGGCATATTTGAACCCGTTGAGTATAAGA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAATTGTAGCGGCTGATTTGCTTAAAGGCGAGCGGGTTATTTTGCAAGAAGGGGACGTTG 15728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGAGCTTATCCGTGTCCTTGCAAAAAAGAAGCGAGTGGAAGAGTTAGACCCACCTGTGC 15788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAGATTCCTTGAGGAAGTTCTCCCCTTACAGGAGAATAGAAAAACTTGAGATACCGACGT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAAATATTATTTGGATTTTACGGTCCCGAAAATGGGGTTTATCGCTGGCCATCGCGTGG 15848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTTTATGCCTCAGGCTACTCCCCTGAAGGGGATGTTCAGCCTTCTGAAGAGGGTAAACT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTACTTGCTCGTTGACGGAGGTATAGTTAACAACCTTCCCGTTGAGCCCTTTCAGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTGTACGGAGCCGGTCATCCAACGGAACATCTGATTCGTTTTGCCAATCTGTTTAAAC 15908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 10410)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                /serotype="0157:H7"
/db_xref="taxon:155
                   gene="narG"
'note="22001"
                                                                                                                                                                                   organism="Escherichia
                                                                                         note="enterohemorrhagic"
                                                                                                                                                               strain="EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (6819),
                                                                                                             xref="taxon:155864"
                                                                        .3970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enterohaemorrhagic Escherichia coli O157:H7 529-533 (2001)
                                                                                                                                                                                   coli
                                                                                                                                                                                                                                                       of Genetics, U
, WI 53706, USA
                                                                                                                                                                                   O157:H7 EDL933"
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                                                                                                                                                                                                                                                                           University
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gene CDS

gene="narH"

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DWYCDLPPASPQTWGEQTDVPESADWYNSSYIIAWGSNVPQTRTPDAHFFTEVRYKGT
KTVAVTDYAEIAKLCDIWLAFKQGTDAMALAMGHWLEREHLDINPSQYFTDYVRRY
TDMPKLIVALEERDGYYAGEAGRACHADAILUDALAGGENNEEWKTVAFWTYAENVAPMGSIG
FRWGEKGKWNLEQRDGKTGEETELQLSLLGSQDEIAEVGFPYFGGDGTEHFNKVELEN
VLLHKLPVRELQLADGSTALVTTVYDLTLAWGLERGLNDVNCATSYDDVKAYTPAWA
EQITGVSRSQIIRIAFAKLOTAMKTHGRSMIIVGGKLHWYHLDMYKGGLINKLIFCG
CVGQSGGWHAHYYGGEKLRFQTGWGPLAFALDWGRPARHMYSTSYFYNHSSQMYFETY
TABELLSPMADKSRYTGHLIDTNVRAERMGWLPSAPQLGTNPLTIAGEAEKAGMNPVD
TVKSLKEGSIRFARAEQPENGKNHPRHLFIRBSNIKGSKSKGETMIKTUNGUN
TVKSLKEGSIRFARAEQPENGKNHPRHLFIRBSNIGGSKGKGHWHYHLDGSIGKHFWKHLTGTHGIN
TVKSLKEGSIRFARAEQPENGKNHPRHLFIRBSNILGSSGKGKGTTHKKNTGTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Residues 1 to 1247 of 1247 are 99.91 pct identical to residues 1 to 1247 of 1247 from Escherichia coli K-12 Strain MG1655: B1224"
                                                                                                                                                                                                                                                                             GKDLGQQGGVKPESVDWQDNGLEGKLDLVVTLDFRLSSTCLYSDIILFTATWYEKDDM
NTSDMHPFIHPLSAAVDPAWEAKSDWEIYKAIAKKFSEVCVGHLGKETDIVTLPIQHD
SAAELAQPLDVKDWKKGECDLIPGKTAPHIMVVERDYPATYERFTSIGPLMEKIGNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVRSTHGVNCTGSCSWKIYVKNGLVTWETQQTDYFRTRPDLPNHEPRGCPRGASYSWY
LYSANRLKYPMMRKRLMKMWREAKALHSDPVBAWASIIEDADKAKSFKQARGRGGFVR
SSWQEVNELIAASNVYTIKNYGPDRVAGFSPIPAMSMVSYASGARYLSLIGGTCLSFY
                                    FLTPHQKWGIHSTYSDNLLMLTLGRGGPVVWLSEADAKDLGIADNDWIEVFNSNGALT
ARAVVSQRVPAGWTWMYHAQERIVNLPGSEITQQRGGIHNSVTRITPKPTHMIGGVAH
                                                                                                                                                                                KGI AMNTQSEMDLLRKLNYTKAEGPAKGQPMLNTA I DAAEMI LTLAPETNGQVAVKAW
AALSEPTGRDHTHLALNKEDEK I RFRD I QAQPRK I I SSP TWSGLEDEHVSYNAGYTNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="nitrate reductase 1,
/protein_id="AAG56084.1"
/db_xref="GI:12514945"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         respiration"
LAYGFNYYGTVGSNRDEFVVVRKMKNIDWLDGEGNDQVQESVK"
                                                                                                                                      HELI PWRTLSGRQQLYQDHQWMRDFGESLLVYRPPIDTRSVKEVIGQKSNGNPEKALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="narG"
/function="enzyme, Energy metabolism,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MSKFLDRFRYFKQKGETFADGHGQLLNTNRDWEDGYRQRWQHDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha subunit
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/note="Residues 1 residues 1 to 512 respiration" 3967. .5505 /gene="narH" function="enzyme; Energy metabolism, carbon: Anaerobic to 512 of 512 are 99.80 pct identical to of 512 from Escherichia coli K-12 Strain

MG1655: B1225"

/codon start=1 /transl_table=11 /product="nitrate reductase 1, /protein_id="AAG56085.1" /db_xref="GI:12514946" beta subunit"

/translation="mkirsqvgmvlmldkcigchtcsvtcknvwtsregveyampnnv etxeeqgeptdwendekykggwirkingkloprmgnamljgkipaphlpgiddyye pededdynlhtapeggksqpiarprslifgrmakiekgpnweddlggepdklakdkn edniqkamysqpentfmyllprlcehclnpacvatcpsgaiykreedgivlidqdkcr gwrmcitgcpykkiyrmwklgrksekcifcyprieagoptvcsetcvgriryldyda adaieraastenekdlyqrqlevfldpndpkvieqaikdgiplsvibaaqqspvykma MEWKLALPLHPEYRTLPMVWYVPPLSPIQSAADAGELGSNGILPDVESLRIPVQYLAN LLTAGDTKPVLRALKRMLAMRHYKRAETVDGKVDTRALEEVGLTEAQAQEMYRYLAIA NYEDRFVVPSSHRELARBAFPBKNGCGFTFGDGCHGSDTKFNLFNSRR I DA I DVTSKT

note="Z2003"

CDS

espiration" function="enzyme; Energy metabolism, carbon: Anaerobic gene="narJ"

/note="Residues 1 residues 1 to 236 /G1655: B1226 of to of 236 are 99.57 from Escherichia identical to i K-12 Strain

transI_table=11

/product="nitrate "unction" reductase 1 delta subunit, assembly

'protein_id="AAG56086.1"

gene

CDS

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Makino, K., Yokoyama, K., Kubota, Y., Yutsudo, C.H., Kimura, S., Kurokawa, K., Ishii, K., Hattori, M., Tatsuno, I., Abe, H., Iida, T., Yamamoto, K., Ohnishi, M., Hayashi, T., Yamamoto, K., Ohnishi, M., Hayashi, T., Yasunaga, T., Honda, T., Sasakawa, C. and Shinagawa, H.

Complete nucleotide sequence of the prophage VT2-Sakai carrying the vertoxini 2 genes of the enterohemorrhagic Escherichia coli O157:H7 derived from the Sakai outbreak

Genes Genet. Syst. 74 (5), 227-239 (1999)
                                        /translation="Mislorkvlrticpdokgliarithicykhelmivqnnbevdhr
Trrppprtelegifndstladxdsladegsyrelmpagrriilyteahtiddld
Mranyggldvelaavighuptlaslverpdipprelygheglsrnehdokmadaldavo
Pdyvvlakynkvlippevysrppnklinihhesplafigarpyhqaysrgvkligatah
vvndnldegpiimqdvihvdhtyttaedmmragrdvervlsraligatah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete nucleotide sequence of the prophage VTI-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli 0157:H7 strain derived from the Sakai outbreak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AP002556 291136 bp DNA linear BCT 07-MAR-2001
Escherichia coli O157:H7 DNA, complete genome, section 7/20.
AP002556 BA000007
AP002556.1 GI:13361156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9766 GCCACCAATITAAGTACTGGGCGTGAATTATGGTTTACTGAAGGCGATCTCCATCTTGCT 9825
                                                                                                                                                                                                                                                                                                                                                                                                                        399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (sites)
Ohnishi, M., Murata, T., Nakayama, K., Kuhara, S., Hattori, M.,
Curokawa, K., Yasunaga, T., Yokoyama, K., Makino, K., Shinagawa, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli O157:H7 (strain:O157:H7, sub_strain:RIMD 0509952)
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9826 ATTCGCGCATCATGCAGTATTCCAGGACTAATGGCACCGTTGCGCATAACGGCTACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comparative analysis of the whole set of rRNA operons between enterchemorrhagic Bscherichia coli 0157:H7 Sakai strain and an Bscherichia coli K-12 strain MG1655 Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                        340 GCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCGGAAGGGAGTTTAATCCCCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTCTCGGCAGCTGTGCAATTCCCGGCATATTTGAACCCGTTGAGTATAAGAATTACTTG
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                                                                                                                                                                                                                                                                                                                        Length 10410;
                                                                                                                                                                                                                                                                                                                                                                        97; Indels
                                                                                                                                                                                                                                                                                                                  6.6%; Score 49.8; DB 1;
52.7%; Pred. No. 0.0014;
tive 0; Mismatches 97;
/protein_id="AAG56089.1"
/db_xref="G1:12514950"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9946 GATATTGTGATAGCGGTCGACCTGC 9970
                                                                                                                                                                                                                                                                       complement (8859. .9317)
                                                                                                                                                                                            complement (8859. .9317)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544
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                                                                                                                                                                                                                    /gene="ychJ"
/note="Z2009"
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Makino, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAGS6088.1"
/db xref="G1:12514949"
/translation="hMVVGGGLLSARFALQVVACGNALSLALESNLSRSFSSRSAWA
NYLFTDSLESSCOTPESDOGGGRIRTFEVDDGRFTVCSLWPLGNPFRGNNFEVMLEMA
VGKGLFVASLLTILRAVACENVLSLESNLSRRFSPPPDECKLSQSHRSYHIAVVNHG
                  /tränslation="MIELVIVSRLLEYPDAALWQHQQBMFBAIAASKNIPKEDAHALG
IPFABULTYMDFLDAQAQYSELPDYGRAYSLLLEHYHGGSRDRQAMADLAQYSEGHG
LQLANSRELPBHLEYLSYLAQAESAVBGLKDIAPILALISARLQQRESRYAVLPDL
LLAKLANTAIDSDKVAEKIADEARDDTPQALDAVWEERQVKFFADKGCGDSAITAHKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="MQFLNMFPPDIYPYIAGAVPLIGSWLRYDYGQYTWRAASSQMLD
KKGMNLASNLFHIGILGIFYGHPFGWLTPHMMYBAWLPIEVKQKMMFAGGASGYLCL
IGGYLLLKRRLFSPRVRATTYGADILILSLLVIQCALGLLTIPFSAQHMDGSEMMKLY
GWAQSVVTFHGGASQHLDGYAFIFRLHLVLGWTLFLLFPFSRLWHIWSVPEYLTRKY
QLVRARH"
                                                                                                                                                                                                                                                                                                                     to 225 of 225 are 99.55 pct identical to of 225 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7247. .7816
//gene="22005"
/function="orf; Unknown function"
/note="Residues 2 to 67 of 189 are 86.36 pct identical to
residues 1 to 66 of 91 from Bscherichia coli K-12 Strain
MGASS5: 81228
                                                                                                                                                                                                                                                                       function="enzyme; Energy metabolism, carbon: Anaerobic
                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
|transl_table=11
|product="nitrate reductase 1, cytochrome b(NR), gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="purU"
function="enzyme; Nucleotide biosynthesis: Purine
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/product="formyltetrahydrofolate deformylase; for
purT-dependent FGAR synthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGRIRTFEVDDGRFTVCSLWPLGNPTTG"
complement (7429. .7513)
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/gene="tyrv"
/product="trNA-Tyr"
/note="anticodon: GTA"
/function="RNA; tRNA;
complement (7723. .7807)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein id="AAG56087.1"
db xref="GI:12514948"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="anticodon: GTA"
/function="RNA; tRNA"
complement (7967. .8809)
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                                                                                                                      PAGAVAPQYLNITTGGQH"
                                                                                                                                                                                                                                                                                                                     /note="Residues 1 residues 1 to 225 MG1655: B1227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Z2005"
7247.
                                                                                                                                                                                              'note="Z2004"
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'note="Z2006"
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                                                                                                                                                                                                                    6212. .6889
/gene="narl"
                                                                                                                                           5212. .6889
/gene="narl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Japan (B-mail:ken@gen-info.osaka-u.ac.jp,
URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365.
Fax:81-6-6879-2047)
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Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 258 (1-2), 127-139 (2000)
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complement(2426. .3280)
/gene="ECs1694"
/note="molybdenum transport protein,similar to molybdenum
                                                                                                                                                                                                                                                                                            DQPTMKALDKQNVAQALSVVPGVVLQKSGSRNBEQVKVRGFDSRQVPVYPDGVPIYVP
YOGKLDLAR ILTNKLGAVEVSKGYSSLLOGPNQMGGALNITTQKCTYKPLEASLGYRQG
WSRSQDNAYDMHAS FAASSELGYLQVSGSQLKQDPLGLFHGVNNDIAGKHGKMINSSA
DDKRGIVKLGPTPRENDEYTLTYIKQDGEKDNEPYSGNSGQKSRYMQNPEXDKESFYY
QGTTQLNDRFTLKSRLYRDTFENTLMMYNSLADLKKKKGSYSHYSDYSDGAGLQLAAD
VRENDLLTFAVNMKDDVHREKGAPHAAYDRYEDRTMSLASEYQMAAADNVDVVAGISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="probable TonB dependent outer membrane receptor receptor, similar to TonB dependent outer membrane receptor PrrA [Escherichia coli CFT073] gi|3661477|gb|AAC61709.1| percent identity 97 in 656 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (430 . .2400)
/gene="ECs1693"
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/gene="ECs1693"
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WLATMFGIGGSIGSRNLHSFLVAVVGAILVLGVFRLLRRB"
                                                                                                                                                 QTMTAWMTLKPWEPLSVTLSEBARSSSYSNSDGSQKAAGFAVTHIRADYTLGHGFSVN
ASVNNLFDTQYAYSBGFVEBGRNFWAGVEYTF"
                                                                                                                                                                                                           DWRDSVEAKKHEKDGSITHYDDNNQSAFNWQVWGKYHFVNEDTLALSYYDRKRFFTLK
ERYTTSKPAYNQIAIVNPQLKPERARGVDLTWNGAFTHDWGFEVSVYYNRVSDAILSH
NIDADTIQNQNSGTVDYSGLDAGIKGKISNILDVGLSYALIHADAKRKDIGKITDLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative TonB dependent outer membrane receptor"
/protein_id="BAB35116.1"
/db_xref="G1:13361158"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
/protein_id="BAB35115.1"
/db_xref="GI:13361157"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
/transl_table=11
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'transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="similar to YMGE_ECOLI gi|1787445 percent identity 7 in 84 aa (Conserved in E.coli K-12)"
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                                                                                             /gene="ECs1694"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MRLKKHYLCTALSLAFTQQAVAAQESDSLTVWSSPVSSTTTTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sub strain="RIMD 0509952"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
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CVSGVSVACKMLTTLGLTIDDAVSDGSQANAGQRLIRAQGNAAALHQGWKAIQNVLEW
SCGVSDYLDQMLALLRERYPDGNIACTRKAIPGTRLLASQAILAAGGLIHRAGCAETI
LLFANHRHFLHDNQDWSGAINQLRRHAPEKKIVVEADTFKEAIAALRAQPDVLQLDKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="unknown,similar to hypothetical proteins e.g. Orf2 [Escherichia coli GFT073] gi[3661479[gb]AAC61711.1] percent identity 98 in 214 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="ECs1696"
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identity 91 in 284 aa"
/note="probable ABC transporter protein (permease),similar.
to ABC transporter permeases e.g. [Haemophilus influenzae]
gi 2501391 | sp | Q57130 | YE71 HAEIN percent identity 40 in 323
                                                                                                                                                                                                                         /translation="mtllavrhaslgysrhpvl;rdvsptlsqgticcllganggktt
lmssilgvipilkgevlldslpvqtlshlgarqalarveqaabgiparsvldwvlmgl
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llldepassldpghqigltdotlaqlknngmymmsthhplhavaiadsiiqvepdgrv
tqglpteqlttnklaalyrvsadqihhhlsaish"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="mLIDDIDFADLYLQQLKLAHRTEKTFDHWDQRAEKMAENCASFT
DSYLQQLIAKIDLQGAQTLFDMGCGFGTVSLALADKLTTIYGVDYSQGMLNVAARRAA
ALKADNVHLIQRAWEEDWSDLFRCDIAVASRSTLVADMRQAMSKLNNQARLRVYTTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (3445. .4089)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       trānslation="MPTLILSVDKIANRITAPRNVLSRTSAGVLARLTTMSVSGYIAG/
INNKMLVPSPLPAATGRSSGGIAYRRRHCDDFPFSGTNRCVTSGRYPGR"
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                                                                                                                                                             complement (4854. .5834)
/gene="ECs1698"
                                                                                                                                                                                                                                                                                                                                                                                   /product="putative ferric enterobactin transport ATP-binding protein" 
/protein id="pAB$120.1" 
/db_xref="GI:13361162"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="probable ferric enterobactin transport similar to ferric enterobactin transport ATP-binding protein [Bacherichia coli (CFT073] gi]3661480[gb|AAC61712.1| percent identity 79 in 148 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (4099. .4857)
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/gene="ECs1697"
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/protein_id="BAB35119.1"
/db_xref="GI:13361161"
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/transl_table=11
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/protein_id="BAB35118.1"
/db_xref="GI:13361160"
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/codon_start=1
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/protein_id="BAB35117.1"
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/transl_table=11
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/transl_table=11
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Search completed: Ju
Job time : 1454 secs
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/evidence=not_experimental
/transl_table=11
/product="putative ABC transporter permease protein"
/protein_id="putative ABC transporter permease protein"
/protein_id="BAB35121.1"
/db xrefe="di1.13361163.1"
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GRQIVFWQIRVPRILAALILGAALAGAGTTYQGMLRNPLVSPDILGVSAGAGLGACTA
ILMGASIYYQLAFGGGALWYNGGWLLTRRVTRRDPLILLVGTALGTAGAGTGACTA
ILMGADFYQLPSITFWLLGGASTVTLRDCYAAPIILLIGSLPEFFRWRMMLLTLSD
DBARSLGIANTTRLRFVGAPTLITASTVAIAGIIGWGLVVPHIARLLTGHNHQQLL
PWAMCTGAILLLLTUTTARSIGTTEIPLGILTAFVGAPPFLLLLIRGGRQ"
/gene="Resident (5834...6856)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47183 GCCACCAATTTAAGTACTGGGCGTGAATTATGGTTTACTGAAGGCGATCTCCATCTTGCT 47242
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Bosl,M. and Kersten,H.
Organization and functions of genes in the upstream region of tyrT of Escherichia coli: phenotypes of mutants with partial deletion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCT 18-MAR-1994
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Escherichia.
                                                                                                                                                                                                                                                                         complement (5834. .6856)
//game=EC81699*
//note="probable ABC transporter, weakly similar to iron (iii) ABC transporter, AIP-binding protein [Pyrococcus (iii) ABC transporter, AIP-binding protein [Pyrococcus (iii)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 CITCICGGCAGCIGIGCAATICCCGGCATATITGAACCCGTIGAGTATAAGAATTACTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 460 CTCGTTGACGGAGGTATAGTTAACAACCTTCCCGTTGAGCCCTTTCAGGAAAGCGGTATT
                                                                                                                                                                                                                                                                                                                                                                           6.6%; Score 49.8; DB 1; Length 291136;
llarity 52.7%; Pred. No. 0.0016;
Conservative 0; Mismatches 97; Indels 0;
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    3653
/organism="Escherichia coli"
/strain="K-12"
    db xref="taxon:562"
    1154 . 1159

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J. Bacteriol. 176 (1), 221-231 (1994)
94110230
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Escherichia coli (strain K-12) DNA.
Escherichia coli
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|524. .2529
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M64675.1 GI:402693
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108; Conserv
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-35 signal
TATA signal
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